

Accession	Sequence	Length
QY	1 GGGGGCCATTCTGTTTCAGCCAGTGGCCAAATTCATTAAGTGGCCAGTGGCAGCACCG	60
Db	1 GGGGGCCATTCTGTTTCAGCCAGTGGCCAAATTCATTAAGTGGCCAGTGGCAGCACCG	60
QY	61 CCAACGCGCGCGGGGGCCACACTGTCGGCTGAAAGCCCGGCAACACAGCGAGCGTCCGG	120
Db	61 CCAACGCGCGCGGGGGCCACACTGTCGGCTGAAAGCCCGGCAACACAGCGAGCGTCCGG	120
QY	121 GCGAGGTGTGGCTGTCTGTCTGAGCAGACGTAAGGACATCTCGCGCTGCGGGGCCCG	180
Db	121 GCGAGGTGTGGCTGTCTGTCTGAGCAGACGTAAGGACATCTCGCGCTGCGGGGCCCG	180
QY	181 GGGCGCGCTGCTGCTGCTGCTGAGCGAGCAGCAGTAAACGTGCTGCTTACGACATGA	240
Db	181 GGGCGCGCTGCTGCTGCTGCTGAGCGAGCAGCAGTAAACGTGCTGCTTACGACATGA	240
QY	241 ACGGCTGTATCTCAAGCCTCAAGGAGCTGGGCCACCTGCCAGAAACGCGAAAGGTGA	300
Db	241 ACGGCTGTATCTCAAGCCTCAAGGAGCTGGGCCACCTGCCAGAAACGCGAAAGGTGA	300
QY	301 GCAAGGTGAGATTCTCCAGACGTCATCGACTACATCAGGGAACCTTCACTGTTGAGCTGA	360
Db	301 GCAAGGTGAGATTCTCCAGACGTCATCGACTACATCAGGGAACCTTCACTGTTGAGCTGA	360

QY 361 ACTCGGAATCCGAAGTGGGACCCCGGGGGCCGAGGGCTGCGGCTCCGGCTCCGCTCA 420
 DB 361 ACTCGGAATCCGAAGTGGGACCCCGGGGGCCGAGGGCTGCGGCTCCGGCTCCGCTCA 420
 QY 421 GACACCTCAACGCGAGATCAAGCCGCTGACGCGCGAGGCGGATGCGTTCGCGGAGC 480
 DB 421 GACACCTCAACGCGAGATCAAGCCGCTGACGCGCGAGGCGGATGCGTTCGCGGAGC 480
 QY 481 ATCGCATCTTGTGTGCTGGAAGCGCTCCCGGAGGACCGCGGAGCCCGCAATCCAGC 540
 DB 481 ATCGCATCTTGTGTGCTGGAAGCGCTCCCGGAGGACCGCGGAGCCCGCAATCCAGC 540
 QY 541 GCGCAGAGGAATTAAGTCTCTGTGTGTGTCTCCCGCAACGCGCTCGCGGATCTGAGG 600
 DB 541 GCGCAGAGGAATTAAGTCTCTGTGTGTGTCTCCCGCAACGCGCTCGCGGATCTGAGG 600
 QY 601 AGAACAGAGCCGATCGCGCGGCACTGCGCCCTTAATCTGATCCAGCTGCGGCTGAGGCT 660
 DB 601 AGAACAGAGCCGATCGCGCGGCACTGCGCCCTTAATCTGATCCAGCTGCGGCTGAGGCT 660
 QY 661 GAGGCACTGCGGAGAGAGGCGGCTCTCTGTCACACCTACTAGTACACAGAGACTTTA 720
 DB 661 GAGGCACTGCGGAGAGAGGCGGCTCTCTGTCACACCTACTAGTACACAGAGACTTTA 720
 QY 721 GGGGGTGGGATCCACCTCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 780
 DB 721 GGGGGTGGGATCCACCTCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 780
 QY 781 TCAAGT 840
 DB 781 TCAAGT 840
 QY 841 CACGCACTGAGATATTTGTTCATTAATAGTCTGTGGGCTGTGTGTGTGTGTGTGTAA 900
 DB 841 CACGCACTGAGATATTTGTTCATTAATAGTCTGTGGGCTGTGTGTGTGTGTGTGTAA 900
 QY 901 AATAATTAGATGTGAAAAA 926
 DB 901 AATAATTAGATGTGAAAAA 926

RESULT 2
 US-09-561-497-10
 / Sequence 10, Application US/09561497
 / Patent No. 6372433
 / GENERAL INFORMATION:
 / APPLICANT: Brenda F. Baker
 / APPLICANT: C. Frank Bennett
 / APPLICANT: Jacqueline Wyatt
 / TITLE OF INVENTION: ANTISENSE MODULATION OF INHIBITOR OF DNA BINDING-1 EXPRESSION
 / FILE REFERENCE: RFS-0149
 / CURRENT APPLICATION NUMBER: US/09/561,497
 / CURRENT FILING DATE: 2000-04-28
 / NUMBER OF SEQ ID NOS: 88
 / SEQ ID NO 10
 / LENGTH: 4793
 / TYPE: DNA
 / ORGANISM: Homo sapiens
 / FEATURE:
 / NAME/KEY: CDS
 / LOCATION: (2210) ... (2659)
 US-09-561-497-10

Query Match 70.0%; Score 648; DB 3; Length 4793;
 Best Local Similarity 78.7%; Pred. No. 1,3e-164;
 Matches 913; Conservative 0; Mismatches 5; Indels 242; Gaps 2;

QY 4 GCCCATCTGTTTACGCAAGTCCGCAAGATCATGAAGTCCGCACTGCGAGCAGCGCA 63
 DB 2178 GCCCATCTGTTTACGCAAGTCCGCAAGATCATGAAGTCCGCACTGCGAGCAGCGCA 2237
 QY 64 CCGCGCGCGCGCGCGCGCGCTGCGCGCTGAAGCGCGCAAGACAGAGACCGTGGCGCG 123

DB 2238 CCGCGCGCGCGCGCGCGCGCTGCGCGCTGAAGCGCGCAAGACAGCGAGCGGTCCGCGC 2297
 QY 124 AGGTGTGCGCTGT 180
 DB 2298 AGGTGTGCGCTGT 2357
 QY 181 GGGCGCGCTGCGCGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTG 240
 DB 2358 GGGCGCGCTGCGCGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTG 2417
 QY 241 AGGCTTTACTCAAGCTCAAGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 300
 DB 2418 AGGCTTTACTCAAGCTCAAGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2477
 QY 301 GCAAGTGTGAATTTCTCAGACGTCATGCACTACATCAGGACCTTCAAGTTGAGCTGA 360
 DB 2478 GCAAGTGTGAATTTCTCAGACGTCATGCACTACATCAGGACCTTCAAGTTGAGCTGA 2537
 QY 361 ACTCGAATCCGAAGTGTGAGACCCCGGGGGCGAGAGGCTGCGGCTCGCGCTCA 420
 DB 2538 ACTCGAATCCGAAGTGTGAGACCCCGGGGGCGAGAGGCTGCGGCTCGCGCTCA 2597
 QY 421 GCAACCTCAACGCGAGATCAAGCGCTCTGAAGCGGCTGCGGCTGCGGCTGCGGCTCA 456
 DB 2598 GCAACCTCAACGCGAGATCAAGCGCTCTGAAGCGGCTGCGGCTGCGGCTGCGGCTCA 2657
 QY 457 ----- 456
 DB 2658 AGATCATCTTATACGAGCGGGGAAACGAGGCGAGAGGCGGTGCGCTTGCACAC 2717
 QY 457 ----- 456
 DB 2718 TTCGTCCTCACTTGGGATCTGCTATGCGGGGCTGCTTGAAGACCTGAAAAAG 2777
 QY 457 ----- 456
 DB 2778 CGCTCCCGGT 456
 QY 457 ----- 456
 DB 2838 TCCAACCCGCGCGCTGCTCATTTCTTCTCGTTTTCACAGCGCGCATGCTGCTGCGAG 2897
 QY 482 TCGCATCTTGT 541
 DB 2898 TCGCATCTTGT 2957
 QY 542 GCGAAGAGAAATTAAGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 601
 DB 2958 GCGAAGAGAAATTAAGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3017
 QY 602 GAACAAGACCGATCGCGCGGCGCACTGCGCCCTTAATCTGATTCAGCTGCGGCTGAG 661
 DB 3018 GAACAAGACCGATCGCGCGGCGCACTGCGCCCTTAATCTGATTCAGCTGCGGCTGAG 3077
 QY 662 AGGCACTGCGAGAGAGAGGCGCTCTCTGCAACCTACTAGTACAGAGACTTTAG 721
 DB 3078 AGGCACTGCGAGAGAGAGGCGCTCTCTGCAACCTACTAGTACAGAGACTTTAG 3137
 QY 722 GGGGTGGGATTCGCTGT 781
 DB 3138 GGGGTGGGATTCGCTGT 3197
 QY 782 CAGGTTGT 841
 DB 3198 CAGGTTGT 3257
 QY 842 ACCGATCGAAGATTTGT 901
 DB 3258 ACCGATCGAAGATTTGT 3317
 QY 902 AATAATTAGATGTGAAAA 921
 DB 3318 AATAATTAGATGTGAAAA 3337

RESULT 3
US-08-151-391A-1
Sequence 1, Application US/08151391A
Patent No. 5527897
GENERAL INFORMATION:
APPLICANT: Oda, Kinichiro
APPLICANT: Nakada, Susumu
APPLICANT: Hara, Eiji
APPLICANT: Yamaguchi, Tomoko
APPLICANT: Nakamura, Takeshi
APPLICANT: Oka, Yumiko
APPLICANT: Kishimoto, Toshihiko
TITLE OF INVENTION: Human ID Genes
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: LOWE, PRICE, LEBLANC & BECKER
STREET: 99 Canal Center Plaza, Suite 300
CITY: Alexandria
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/151,391A
FILING DATE: 12-NOV-1993
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: M118, Demetra J.
REGISTRATION NUMBER: 34,506
REFERENCE/DOCKET NUMBER: 715-087
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 684-1111
TELEFAX: (703) 684-1124
TELEX: 82-4425
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 509 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: 22,483
OTHER INFORMATION: /note= "CDS"
US-08-151-391A-1

Query Match 52.7%; Score 488.4; DB 1; Length 509;
Best Local Similarity 98.6%; Pred. No. 4,3e-122;
Matches 503; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

QY 15 TTCAGCCAGTGGCCCAAGATCATGAAAGTCCGACATGGGACGACCGCCACCGCCCGCG 74
DB 1 TTCAGCCAGTGGCCCAAGATCATGAAAGTCCGACATGGGACGACCGCCACCGCCCGCG 60

QY 75 GAGCCCAAGCTGGCGCTGAAGGCGGCAAGACAGGAGCGGTGCGGGCGAGGTGGTGGCG 134
DB 61 GAGCCCAAGCTGGCGCTGAAGGCGGCAAGACAGGAGCGGTGCGGGCGAGGTGGTGGCG 120

QY 135 TGTCTGTCTGACAGAGCGTGGCCATCTTGGCGCTGCCGGGGCGCCGGGGCGGCTGTGCT 194
DB 121 TGTCTGTCTGACAGAGCGTGGCCATCTTGGCGCTGCCGGGGCGCCGGGGCGGCTGTGCT 180

QY 195 GCCCTGCTGAGCGAGCAGAGTAAGCTGCTGCTCTACGACATGAAAGGCTGTACTCA 254
DB 181 GCCCTGCTGAGCGAGCAGAGTAAGCTGCTGCTCTACGACATGAAAGGCTGTACTCA 240

QY 255 CGCCTCAAGAGAGCTGTGCTCCACCTGCTCCCGAAGACCGCAAGGTGAGGAGATT 314
DB 241 CGCCTCAAGAGAGCTGTGCTCCACCTGCTCCCGAAGACCGCAAGGTGAGGAGATT 300

QY 315 CTCACAGCGATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 374
DB 301 CTCACAGCGATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 360

QY 375 GTTGGAGACCCCGGGGGGGCGAGGGCTGCGGGTCCGGCTCGAGACCCCTCAAGGCG 434
DB 361 GTTGGAGACCCCGGGGGGGCGAGGGCTGCGGGTCCGGCTCGAGACCCCTCAAGGCG 420

QY 435 GAGATCAGCGCCTGACCGCGCGAGCGGACGATGCTTCTGCGGACGATCATCTTGTGT 494
DB 421 GAGATCAGCGCCTGACCGCGCGAGCGGACGATGCTTCTGCGGACGATCATCTTGTGT 480

QY 495 CGCTGAAGCGCTCTCCCGAAGGACCGGCGG 524
DB 481 CGCTGAAGCGCTCTCCCGAAGGACCGGCGG 509

RESULT 4
US-08-896-164-30
Sequence 30, Application US/08896164
Patent No. 6218521
GENERAL INFORMATION:
APPLICANT: OBATA, Yuichi
TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES ASSOCIATED
TITLE OF INVENTION: WITH GASTRIC CANCER AND METHODS FOR
TITLE OF INVENTION: DIAGNOSING AND TREATING GASTRIC CANCER
NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44mb
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/896,164
FILING DATE: July 17, 1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: No. 6218521man D. Hanson
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5499 - JEL/NDH/SLH
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 721 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-896-164-30

Query Match 47.8%; Score 442.2; DB 3; Length 721;
Best Local Similarity 95.1%; Pred. No. 1.5e-109;
Matches 466; Conservative 0; Mismatches 21; Indels 3; Gaps 1;

QY 4 GCCCATCTGTTTACGACGATGCGCAAGATCATGAAAGTCCGACGATGGACACCGCCA 63
DB 31 GCCCATCTGTTTACGACGATGCGCAAGATCATGAAAGTCCGACGATGGACACCGCCA 90

QY 64 CCGCCGCGCGGAGCCGAGCTGGGCGTGAAGCGCCGCAAGACAGCGAGCGGCGCGCG 123
DB 91 CCGCGCGCGCGGAGCCGAGCTGGGCGTGAAGCGCCGCAAGACAGCGAGCGGCGCGCG 150
QY 124 AGGTGTGTGCGGTGTCTGTCTGAGCAGAGCGGTGCGCATCTGCGCGT---CCGAGGCGCGG 180
DB 151 AGGTGTGTGCGGTGTCTGTCTGAGCAGAGCGGTGCGCATCTGCGCGTCCGCGGAGCGCGG 210
QY 181 GGGGCGCGCTGCGCGTGTCTGTCTGAGCAGAGCGGTGCGCATCTGCGCGTCTTACGACATGA 240
DB 211 GGGGCGCGCTGCGCGTGTCTGTCTGAGCAGAGCGGTGCGCATCTGCGCGTCTTACGACATGA 270
QY 241 ACCGCTGTACTACGCGCTCAAGAGAGTGTGCGCGACCGCGCGCGCAAGCGCGAGTGA 300
DB 271 ACCGCTGTACTACGCGCTCAAGAGAGTGTGCGCGACCGCGCGCGCAAGCGAGTGA 330
QY 301 GCAAGGTGAGATTTCTTCAGCAGCAGTCACTCACTACATCAAGGACCTTCAAGTGTGAGCTGA 360
DB 331 GCAAGGTGAGATTTCTTCAGCAGCAGTCACTCACTACATCAAGGACCTTCAAGTGTGAGCTGA 390
QY 361 ACTCGGATTCGAGATTTGGAGACCGCGGAGCGCGAGCGCGTGTGCGCGCGCTTCCGCTCA 420
DB 391 ACTCGGATTCGAGATTTGGAGACCGCGGAGCGCGAGCGCGTGTGCGCGCGCTTCCGCTCA 450
QY 421 GCAAGGTGAGATTTCTTCAGCAGCAGTCACTCACTACATCAAGGACCTTCAAGTGTGAGCTGA 480
DB 451 GCAAGGTGAGATTTCTTCAGCAGCAGTCACTCACTACATCAAGGACCTTCAAGTGTGAGCTGA 510
QY 481 ATGCACTCTT 490
DB 511 ANATCATCTT 520

RESULT 5

US-08-151-391A-3
Sequence 3, Application US/08151391A
Patent No. 5527897

GENERAL INFORMATION:

APPLICANT: Oda, Kinichiro
APPLICANT: Nakada, Susumu
APPLICANT: Hara, Eiichi
APPLICANT: Yamaguchi, Tomoko
APPLICANT: Nakamura, Takeshi
APPLICANT: Oka, Yumiko
APPLICANT: Kishimoto, Toshihiko
TITLE OF INVENTION: Human ID Genes
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: LOWE, PRICE, LEBLANC & BECKER
STREET: 99 Canal Center Plaza, Suite 300
CITY: Alexandria
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/151,391A
FILING DATE: 12-NOV-1993
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Mills, Demetra U.
REGISTRATION NUMBER: 34,506
REFERENCE/DOCKET NUMBER: 715-087
TELEPHONE: (703) 684-1111
TELEFAX: (703) 684-1124
TELEX: 82-4425
INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
LENGTH: 502 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: misc feature
LOCATION: 22..465
OTHER INFORMATION: /note= "CDS"
US-08-151-391A-3

Query Match 47.6%; Score 440.8; DB 1; Length 502;
Best Local Similarity 95.4%; Pred. No. 2,9e-109;
Matches 454; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 15 TTCAGCCAGTTCGCCAGATCATGAAAGTCCAGTGGCAGCACCGCCGCGCGG 74
DB 1 TTCAGCCAGTTCGCCAGATCATGAAAGTCCAGTGGCAGCACCGCCGCGCGG 60
QY 75 GCGCCAGCTGCGCGCTGAAGGCGCGCAGACAGCGAGCGGTGCGCGCGAGTGTGCGC 134
DB 61 GCGCCAGCTGCGCGCTGAAGGCGCGCAGACAGCGAGCGGTGCGCGCGAGTGTGCGC 120
QY 135 TGTCTGTCTGAGAGAGCGGTGCGCATCTGCGCTGCGCGGCGCGCGCGCGCTT 194
DB 121 TGTCTGTCTGAGAGAGCGGTGCGCATCTGCGCTGCGCGGCGCGCGCGCGCTT 180
QY 195 GCGCTGTGAG 254
DB 181 GCGCTGTGAG 240
QY 255 CCGCTCAAGAGAGTGTGCGCACCGCTGCGCGCAGAACCGCAGAGTGAAGAGAGATT 314
DB 241 CCGCTCAAGAGAGTGTGCGCACCGCTGCGCGCAGAACCGCAGAGTGAAGAGAGATT 300
QY 315 CTCAGCAGTGCATGATCATGATCATGATCATGATCATGATCATGATCATGATCAT 374
DB 301 CTCAGCAGTGCATGATCATGATCATGATCATGATCATGATCATGATCATGATCAT 360
QY 375 GTTGGAGCGCGCGGCGCGAGAGGCGCGGTGCGCGGTGCGCGGTGCGCGGTGCGCG 434
DB 361 GTTGGAGCGCGCGGCGCGAGAGGCGCGGTGCGCGGTGCGCGGTGCGCGGTGCGCG 420
QY 435 GAGATCAGCGCGCTTCAAGCGCGCGAGCGCGAGTGTGCGCGAGTGTGCGCATCTT 490
DB 421 GAGATCAGCGCGCTTCAAGCGCGCGAGCGCGAGTGTGCGCGAGTGTGCGCATCTT 476

RESULT 6

US-08-896-164-31/C
Sequence 31, Application US/08896164
Patent No. 6218521

GENERAL INFORMATION:

APPLICANT: OBARA, YUICHI
TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES ASSOCIATED
TITLE OF INVENTION: WITH GASTRIC CANCER AND METHODS FOR
TITLE OF INVENTION: DIAGNOSING AND TREATING GASTRIC CANCER
NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44mb
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/896,164
FILING DATE: July 17, 1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: No. 6218521man D. Hanson
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5499 - JEL/NDH/SLH
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 461 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-896-164-31

Query Match 36.9%; Score 341.6; DB 3; Length 461;
Best Local Similarity 79.3%; Pred. No. 1.6e-82;
Matches 365; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

QY 457 AGCGCGCATGCGCTCTCTCGCGAGCATCGCATCTTGTCGTGAAGCGCTCCCGCAGG 516
DB 461 AGCGCGCANGGCTTCTGCGAGCATCTTGTCGTGAAGCGCTCCCGCAGG 402
QY 517 ACCGCGGAGCCCGCAGCATTCAGGGGGCAGAGGAATTAAGTCTCTGTGGGCTCCCGC 576
DB 401 ACCGCGGAGCCCGCAGCATTCAGGGGGCAGAGGAATTAAGTCTCTGTGGGCTCCCGC 342
QY 577 AACGGCGCTCGCGCGGATCTGAGGAGAAACAAGCCGATCGGGGCACTGCGCCCTTAC 636
DB 341 NAAAGGCCCTGCGGATTTGGAGAGGAGNAGNCCGATTGGCGCAATGNGCCCTTAA 282
QY 637 TGCATCCAGCCTGCGGCTGAGGCTGAGGCACTGCGGAGGAGGCGCTCTCTGAC 696
DB 281 TGNATNCAGCCTGCGGAGTNGAGTGAAGCAATGAGNGAGGAGGAGGCTTTTGAN 222
QY 697 ACTTACTAGTACCAAGACCTTTAGGGGGTGGGATTCACCTGCTGTTCTATTATTTTG 756
DB 221 ACTTACTAGTACCAAGACCTTTAGGGGGTGGGATTCACCTGCTGTTCTATTATTTTG 162
QY 757 AAAACGACATTTTAAAAATGTCACCTTGGCTCTCAATTTCTGAGAAATG 816
DB 161 NAAACGACAAATTTAAAAATGTTAAAGTGTGTTTAAATTTTGGGGAATG 102
QY 817 CTTGTATTTATTTATTAACATGATCAGCAGCTGAGATTTGTTTACAAATGTTCTG 876
DB 101 NTTTGTATTTGTAATTAACANAGTACCGANTGGAATATTTGTTTACATATGTTTGTG 42
QY 877 GGGCTGTTTTTTTGTATTAAACAATAATTTAGATGTTG 916
DB 41 GGGGTGTTTTTTTGTATTAAANNAATTAATTAATGTTG 2

RESULT 7
US-09-513-999C-13300
Sequence 13300, Application US/0951399C
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclerc, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
FILE REFERENCE: 59, US2, REG
CURRENT APPLICATION NUMBER: US/09/513, 999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent. pm

SEQ ID NO 13300
LENGTH: 171
TYPE: DNA
ORGANISM: Homo sapiens
US-09-513-999C-13300

Query Match 9.6%; Score 89; DB 4; Length 171;
Best Local Similarity 99.0%; Pred. No. 1.2e-14;
Matches 100; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 4 GCCATTCTGTTTACGACCGAGTCGCCAAGATCATGAAGTCCGCGTGCAGCAGCAGCA 63
DB 72 GCCATTCTGTTTACGACCGAGTCGCCAAGATCATGAAGTCCGCGTGCAGCAGCAGCA 131
QY 64 CCG 104
DB 132 CCG 171

RESULT 8

US-08-256-077-3
Sequence 3, Application US/08256077
Patent No. 5654188

GENERAL INFORMATION:
APPLICANT: Elmeyer, Wilfried
TITLE OF INVENTION: Neuroblastoma-Associated Regulator Gene
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3934

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,077
FILING DATE: 23-JUNE-1994

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 0652,1360000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
LENGTH: 360 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-256-077-3

Query Match 8.1%; Score 75; DB 1; Length 360;
Best Local Similarity 58.0%; Pred. No. 1.1e-10;
Matches 163; Conservative 0; Mismatches 100; Indels 18; Gaps 1;

QY 91 TGAAGCGCGGAGCAGCAGCGGTGCGGCGAGGTGCTGCTGCTGAGCAGA 150
DB 2 TGAAGCGCGTGAAGCGCGGTGCGGCGGTGCTGAGAGCGGTGCTGCTGAGCAGA 61
QY 151 GGTGCGCATCTCGCGCTGCGGCGCGCGCGCGCGCGCGCTGCTGCTGAGCAGC 210
DB 62 GCTGCGCATCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGAGAGCGCTGAGACT 118
QY 211 AGCAGGTAAAGTGTCTCTACGACATGAACGCGCTTACTCAGCGCTCAAGAGAGCTGG 270

Db 119 -----TCTGACGACATGAACCACTCTCTCCCGCTGGGAACTG 163
QY 271 TGCCACCCCTGCCGACAGCCGCAAGGTGAGATTTCTCCAGACGTATCG 330
Db 164 TACCCGAGATCCGAGAGGCACTCAGCTTAGCCAGGTGGAATCTTACAGCGGTATCG 223
QY 331 ACTACATCAGGACCTTCAGTTGAGCTGAACCTCGAATCC 371
Db 224 ACTACATTTCTGACCTGACGTAGTCTCTGCGCGAGCCAGCC 264

RESULT 9
US-08-466-127-3
; Sequence 3, Application US/08466127
; Patent No. 5683878
; GENERAL INFORMATION:
; APPLICANT: Elimeier, Wilfried
; TITLE OF INVENTION: Neuroblastoma-Associated Regulator Gene
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,127
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 0652.1360002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; NAME/KEY: CDS
; LOCATION: 1..357
; US-08-466-127-3

Query Match 8.1%; Score 75; DB 1; Length 360;
Best Local Similarity 58.0%; Pred. No. 1.1e-10;
Matches 163; Conservative 0; Mismatches 100; Indels 18; Gaps 1;

QY 91 TGAAGCCGCGCAACAGACGAGCGAGCGGCGGCGGTGCGCTGTCTCTGAGACGA 150
Db 2 TGAAGCGGCTGAGCCCGGTGCGGCGGCTGTACGAGCGGCTGTCTGTGGAACGCA 61
QY 151 GCGTGGCCATCTCGCGCTGCGCGGCGCGCCGAGGCGCGCTGCGCTTCTGAGACG 210
Db 62 GCTGCGCCATCTCGCGGCGCGGAGGAGGCGCGGCAAGCTGAGAGCGGCTAGCT--- 118
QY 211 AGCAGTAAAGTGTGCTCTACGACATGAACGGCTTTACTACGCGCTTCAAGAGCTG 270
Db 119 -----TCTGACGACATGAACCACTCTCTCCCGCTGGGAACTG 163
QY 271 TGCCACCCCTGCCGACAGCCGCAAGGTGAGATTTCTCCAGACGTATCG 330

Db 164 TACCCGAGATCCGAGAGGCACTCAGCTTAGCCAGGTGGAATCTTACAGCGGTATCG 223
QY 331 ACTACATCAGGACCTTCAGTTGAGCTGAACCTCGAATCC 371
Db 224 ACTACATTTCTGACCTGACGTAGTCTCTGCGCGAGCCAGCC 264

RESULT 10
US-08-256-077-1
; Sequence 1, Application US/08256077
; Patent No. 5654188
; GENERAL INFORMATION:
; APPLICANT: Elimeier, Wilfried
; TITLE OF INVENTION: Neuroblastoma-Associated Regulator Gene
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/256,077
; FILING DATE: 23-JUNE-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 0652.1360000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 982 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-256-077-1

Query Match 8.1%; Score 75; DB 1; Length 982;
Best Local Similarity 58.0%; Pred. No. 1.8e-10;
Matches 163; Conservative 0; Mismatches 100; Indels 18; Gaps 1;

QY 91 TGAAGCCGCGCAACAGACGAGCGGCGGCGGCGGTGCGCTGTCTCTGAGACGA 150
Db 125 TGAAGCGGCTGAGCCCGGTGCGGCGGCTGTACGAGCGGCTGTCTGTGGAACGCA 184
QY 151 GCGTGGCCATCTCGCGCTGCGCGGCGCGCCGAGGCGCGCTTCTGAGACG 210
Db 185 GCTGCGCCATCTCGCGGCGCGGAGGAGGCGCGGCAAGTGAAGAGCGGCTAGCT--- 241
QY 211 AGCAGTAAAGTGTGCTCTACGACATGAACGGCTTTACTCAAGCTTCAAGAGCTG 270
Db 242 -----TCTGACGACATGAACCACTCTCTCTCCCGCTGGGAACTG 286
QY 271 TGCCACCCCTGCCGACAGCCGCAAGGTGAGATTTCTCCAGACGTATCG 330
Db 287 TACCCGAGATCCGAGAGGCACTCAGCTTAGCCAGGTGGAATCTTACAGCGGTATCG 346
QY 331 ACTACATCAGGACCTTCAGTTGAGCTGAACCTCGAATCC 371
Db 347 ACTACATTTCTGACCTGACGTAGTCTCTGCGCGAGCCAGCC 387

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RESULT 11
US-08-466-127-1
; Sequence 1, Application US/08466127
; Patent No. 5683878
; GENERAL INFORMATION:
; APPLICANT: Ellmeier, Willfried
; APPLICANT: Weith, Andreas
; TITLE OF INVENTION: Neuroblastoma-Associated Regulator Gene
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESSES:
; ADDRESSES: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,127
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 0652.1360002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 982 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 37..481
;
US-08-466-127-1
Query Match 8.1%; Score 75; DB 1; Length 982;
Best Local Similarity 58.0%; Pred. No. 1.8e-10;
Matches 163; Conservative 0; Mismatches 100; Indels 18; Gaps 1;

QY 91 TGAAGCGCGGCAAGACAGGAGCGGTGCGGCGGAGGTGCGCTGTCTGTCTAGACAGA 150
DB 125 TGAAGCGCGTGAGCGCGGTGCGGCGCTGCTACGAGCGGCTGTCTGTCTGTGGAACCA 184
QY 151 GGTGGCCATCTGCGGCTGCGGCGGCGCGGCGGCGCTGCTGCGCCCTGCGAGCGAGC 210
DB 165 GTCTGCGCATCGCGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 241
QY 211 AGCAGTAAACGTGCTGTCTACGACATGAAACGCTGTACTACGCGCTCAAGAGCTGG 270
DB 242 -----TGCTGAGACGACATGAAACGCTGTACTGCGCGCGGCGGCGGCGGCGGCGGCGG 286
QY 271 TGCCCAACCTGCGCCCAAGACCGCAAGGTGAGCAAGGTGAGATTCTCCAGACGTCATCG 330
DB 287 TACCGCGAGTCCCGAGAGCGACTGAGCTTAGCGAGGTGAAATCTTACAGCGCGTCATCG 346
QY 331 ACTACATCAGGACCTTCACTGAGCTGAGCTGAATCGAATCC 371
DB 347 ACTACATTTCTGACCTGAGGTAGTATCTGCGCGAGCGCACCC 387
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RESULT 12
US-09-621-976-2005
; Sequence 2005, Application US/09621976
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; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Mline Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 2005
; LENGTH: 626
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 211..570
; NAME/KEY: sig_peptide
; LOCATION: 211..378
; OTHER INFORMATION: Von Heijne matrix
; OTHER INFORMATION: score 3.5999990463257
; OTHER INFORMATION: seq LQIALGLAXPLX/DL
US-09-621-976-2005
Query Match 7.8%; Score 72; DB 4; Length 626;
Best Local Similarity 77.9%; Pred. No. 9.3e-10;
Matches 95; Conservative 3; Mismatches 23; Indels 1; Gaps 1;

QY 227 GCTCTACGACATGAGCGGCTGTACTCAGCGCTCAGAGAGGTGTGCCACCTGCCCCA 286
DB 220 KSTATACACATGAGACGCTGTCTACTCAAGCTCAAGAGCTGTGGCCACGATCCCCA 279
QY 287 GAACCGCAAGGTGAGCAAGGTGAGATTTCACGACGT-CATGACTTACATCAGGAGCC 345
DB 280 GACAGAGAGGTGAGCAAGATGAAATCTCTGACGACGTCATGACTATCATCTTGGGAC 339
QY 346 TT 347
DB 340 CT 341

RESULT 13
US-08-642-255-48
; Sequence 48, Application US/08642255
; Patent No. 5773249
; GENERAL INFORMATION:
; APPLICANT: CARPILLO, Joseph A.
; APPLICANT: FERRARI, Franco A.
; TITLE OF INVENTION: High Molecular Weight Collagen-Like
; NUMBER OF SEQUENCES: 135
; CORRESPONDENCE ADDRESSES:
; ADDRESSES: FLEHR, HOEBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/642,255
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: ROWLAND, Beirtram I.
; REGISTRATION NUMBER: 20,015
; REFERENCE/DOCKET NUMBER: A55556-3/BIR
; TELECOMMUNICATION INFORMATION:
```

TELEPHONE: (415) 494-8700
TELEFAX: (415) 494-8771
TELEX: 910 277299 FHT UR
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 432 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic"
US-08-642-255-48

Query Match 5.4%; Score 50; DB 1; Length 432;
Best Local Similarity 50.0%; Pred. No. 0.00066;
Matches 152; Conservative 0; Mismatches 150; Indels 2; Gaps 1;

QY 51 GGCAGCACCCGACCCGCGCGCGCCGAGCTGCGCTGAAGCCGCGCAAGACAGCG 110
DB 123 GGCCTGCTCCACCGGGTGTCTCCGGACCTGCAAGCCCGCCAGGTGCGCTGAGACCGGCTGG 182
QY 111 AGCGGTGCGGCGAGGTGTGCTGTCTGTGAGAGAGCGTGGCCATCTCGCGCTGC 170
DB 183 TCCACCGGGTGTCTCCGGACCTGCAAGCCCGCCAGGTGCGCTGAGACCGGCTGTCCACC 242
QY 171 CGGGGCGCGGGGCGCGCTGCTGCGC--CTGCTGAGACGAGAGAGGTAACGTGCTGC 228
DB 243 GGGTGTCTCCGGACCTGCAAGCCCGCCAGGTGCGCGCTGAGACCGGCTGTCCACCGGGTGC 302
QY 229 TCTACGACATGAAGCGCTGTACTCAAGCTCAAGAGAGCTGTGCCACCTGTGCCAGAGA 288
DB 303 TCCGGAGACTGACAGGCCCGCCAGAGTGGCGCTGGAACCGGCTGTGTCACCGGGTGTCCGGG 362
QY 289 ACCGCAAGTGAAGCAAGTGTGAATCTCCAGCAAGTGTATGACTACATCAAGGACCTTC 348
DB 363 ACCGTGAGGCCCGCCAGGTGCCATGTGCCAGAGCCAGAGACCGAAGAGACTCAAGGTCCGGC 422
QY 349 AGTT 352
DB 423 AGGT 426

RESULT 14
US-08-642-255-50
Sequence 50, Application US/08642255
Patent No. 5773349
GENERAL INFORMATION:
APPLICANT: CAPELLI, Joseph
APPLICANT: FERRARI, Franco A.
TITLE OF INVENTION: High Molecular Weight Collagen-Like
TITLE OF INVENTION: Protein Polymers
NUMBER OF SEQUENCES: 135
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOEBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/642,255
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ROWLAND, Bertram I.
REGISTRATION NUMBER: 20,015
REFERENCE/DOCKET NUMBER: A5556-3/BIR
TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 494-8700
TELEFAX: (415) 494-8771
TELEX: 910 277299 FHT UR
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 756 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic"
US-08-642-255-50

Query Match 5.4%; Score 50; DB 1; Length 756;
Best Local Similarity 50.0%; Pred. No. 0.00088;
Matches 152; Conservative 0; Mismatches 150; Indels 2; Gaps 1;

QY 51 GGCAGCACCCGACCCGCGCGCGCCGAGCTGCGCTGAAGCCGCGCAAGACAGCG 110
DB 447 GGCCTGCTCCACCGGGTGTCTCCGGACCTGCAAGCCCGCCAGGTGCGCTGAGACCGGCTGG 506
QY 111 AGCGGTGCGGCGAGGTGTGCTGTCTGTGAGAGAGCGTGGCCATCTGCGCTGC 170
DB 507 TCCACCGGGTGTCTCCGGACCTGCAAGCCCGCCAGGTGCGCTGAGACCGGCTGTCCACC 566
QY 171 CGGGGCGCGGGGCGCGCTGCTGCGC--CTGCTGAGACGAGAGAGGTAACGTGCTGC 228
DB 567 GGGTGTCTCCGGACCTGCAAGCCCGCCAGGTGCGCGCTGAGACCGGCTGTCCACCGGGTGC 626
QY 229 TCTACGACATGAAGCGCTGTACTCAAGCTCAAGAGAGCTGTGCCACCTGTGCCAGAGA 288
DB 627 TCCGGAGACTGACAGGCCCGCCAGAGTGGCGCTGGAACCGGCTGTGTCACCGGGTGTCCGGG 686
QY 289 ACCGCAAGTGAAGCAAGTGTGAATCTCCAGCAAGTGTATGACTACATCAAGGACCTTC 348
DB 687 ACCGTGAGGCCCGCCAGGTGCCATGTGCCAGAGGACCGAAGAGACTCAAGGTCCGGC 746
QY 349 AGTT 352
DB 747 AGGT 750

RESULT 15
US-09-252-991A-8086
Sequence 8086, Application US/09252991A
Patent No. 6531795
GENERAL INFORMATION:
APPLICANT: MARC J. RUBENFIELD et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196, 136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 8086
LENGTH: 969
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-8086

Query Match 5.2%; Score 47.8; DB 4; Length 969;
Best Local Similarity 46.5%; Pred. No. 0.0039;
Matches 154; Conservative 0; Mismatches 177; Indels 0; Gaps 0;

QY 33 ATCATGAAAGTCCGACGTGACAGACCGCCGCGCGCGCCCGAGCTGCGGCTG 92
DB 163 ATGAGAACTCCCGCCATCAACCGCCCTGCGCTGTGATCTCCGCGCGCCAG 222
QY 93 AAGCGCGGCAAGACAGAGCGGCTGCGGGGAGAGTGTGTGTGTGAGCAGAGC 152

Db	223	GC	CG	AC	CG	CT	CG	AG	CA	TC	CG	CA	AG	CG	CG	GT	AT	TG	CG	CG	GT	CG	CG	TC	TC	GC	AG	CG	282
QY	153	GT	GC	CA	AT	CT	CG	CG	CT	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	212	
Db	283	AA	CC	CG	CG	CT	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	342	
QY	213	CA	GT	AA	CG	TC	CT	TA	CG	CA	TC	GA	TC	GA	TC	GA	TC	GA	TC	GA	TC	GA	TC	GA	TC	GA	TC	272	
Db	343	TA	TG	CC	AA	GG	CC	CT	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	402	
QY	273	CC	CA	CC	TC	GC	CC	CA	AG	CG	CA	AG	CG	CA	AG	CG	CA	AG	CG	CA	AG	CG	CA	AG	CG	CA	AG	332	
Db	403	GC	CA	AC	CG	AT	CC	CG	CT	CG	CT	GA	CG	CG	GA	CA	AG	GT	CG	AC	CT	GT	CT	CG	CG	CA	AT	462	
QY	333	TA	CA	TC	CA	GG	GA	CC	TT	CA	GT	TC	GA	CT	GA	CT	GA	CT	GA	CT	GA	CT	GA	CT	GA	CT	GA	363	
Db	463	AT	CA	CC	CG	GA	CG	GT	CG	CG	AG	CA	GG	GT	GA	CT	GA	CT	GA	CT	GA	CT	GA	CT	GA	CT	GA	493	

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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Title: US-09-996-529A-4
Perfect score: 926
Sequence: 1 ggggccattctgttccagc.....ttagatcgtggaaaaaaaaaa 926

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues
Total number of hits satisfying chosen parameters:

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing:  Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
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2:  gb_hcg:*
3:  gb_in:*
4:  gb_om:*
5:  gb_ov:*
6:  gb_pat:*
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8:  gb_pl:*
9:  gb_pr:*
10: gb_ro:*
11: gb_scb:*
12: gb_ey:*
13: gb_un:*
14: gb_vi:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	926	100.0	926	6	C0776735	C0776735 Sequence
2	926	100.0	926	6	AR206583	AR206583 Sequence
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4	926	100.0	926	9	HS1d1	X77956 H.sapiens I
5	905.2	97.8	981	9	BC000613	BC000613 Homo sapi
6	905.2	97.8	993	9	BC012420	BC012420 Homo sap
7	897	96.9	924	6	C0726305	C0726305 Sequence
8	648	70.0	4793	9	AR206590	AR206590 Sequence
9	648	70.0	4793	9	HSU57645	U57645 Human helix
10	648	70.0	146574	2	AC023455	AC023455 Homo sapi
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14	488.4	52.7	509	6	I22507	I22507 Sequence 1
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19	460.2	49.7	99593	9	HS4877M1.7	AL117381 Human DNA

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21	446.8	48.3	468	9	BT007443	BT007443 Homo sapi
22	446.8	48.3	468	12	BT008282	BT008282 Synthetic
23	444	47.9	502	9	HUMID1HB	D13590 Homo sapien
24	442.2	47.8	721	6	ARI46590	ARI46590 Sequence
25	442.2	47.8	721	6	BD079839	BD079839 Cancer-as
26	441	47.6	79419	9	HS0324017	AL110115 Human DNA
27	440.8	47.6	502	6	E07537	E07537 Human id ge
28	440.8	47.6	502	6	I22508	I22508 Sequence 3
29	434	46.9	925	10	BC025073	BC025073 Mus muscu
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31	424.8	45.9	927	6	AX305509	AX305509 Sequence
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33	416	44.9	426	11	G07231	G07231 human STS W
34	409.8	44.3	909	10	RATD125A	M86708 Rattus norv
35	392.8	42.4	81171	2	AC016218	AC016218 Homo sapl
36	341.6	36.9	461	6	ARI46591	ARI46591 Sequence
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38	334	36.1	660	10	RATD1	D10862 Rattus norv
39	300.8	32.5	65959	2	AC024144	AC024144 Mus muscu
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41	298	32.2	224942	2	AC024362	AC024362 Mus muscu
42	296.4	32.0	749	10	MNU43884	U43884 Mus musculu
43	289	31.2	1124	6	AX401898	AX401898 Sequence
44	289	31.2	1124	6	AX827472	AX827472 Sequence
45	289	31.2	1124	10	RATD125A	L23148 Rattus norv

ALIGNMENTS

RESULT 1					
LOCUS	C0776735	926 bp	DNA	linear	PAT 11-MAR-2000
DEFINITION	Sequence 421 from Patent EP1394274.				
ACCESSION	C0776735				
VERSION	C0776735.1	GI:45380125			
KEYWORDS					
SOURCE					
ORGANISM	Homo sapiens (human)				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.				
REFERENCE	1 Ohtani,N., Sugita,Y., Yamaya,M., Kubo,H., Nagai,H. and Izuhashi,K. Method of testing for bronchial asthma or chronic obstructive pulmonary disease Patent: EP 1394274-A 421 03-MAR-2004;				
JOURNAL	Genox Research, Inc. (JP)				
FEATURES	Location/Qualifiers				
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	/mol_type="unassigned DNA"				
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ORIGIN					
Query Match	100.0%	Score 926;	DB 6;	Length 926;	
Best Local Similarity	100.0%	Pred. No. 8.8e-174;			
Matches 926;	Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0
Oy	1	GGGGCCCATTCGTGTTTCAGCCAGTCGCGCAAGATCATGAAATCGCCAGTGCAGACCG	60		
Db	1	GGGGCCCATTCGTGTTTCAGCCAGTCGCGCAAGATCATGAAAGTCGCAATGGCAGACCG	60		
Oy	61	CCACCGCCCGCGGGGGCCCCAGCTGCGCGCTGAAGCGCCGCAAGACAGAGCGAGCTGGCGG	120		
Db	61	CCACCGCCCGCGGGGGCCCCAGCTGCGCGCTGAAGCGCCGCAAGACAGAGCGAGCTGGCGG	120		
Oy	121	GCGAGTGTGTGCGTGTCTGTCTGAGCAGAGGCTGGCCATCTCGCGCTCCGGGGGCGCG	180		
Db	121	GCGAGTGTGTGCGTGTCTGTCTGAGCAGAGGCTGGCCATCTCGCGCTCCGGGGGCGCG	180		
Oy	181	GGGCGCGCTGCTGCTCCCTGCTGACGAGCAGACAGGTAACGTGCTGCTTACGACATGA	240		

Db	181	GGGGCGCGCTCCCTCCCTCTGCTGAGCAGACGAGGTAAACGTGCTCTCTACGACATGA	2448
Qy	241	ACGGCTGTACTACGCGCTTCAGAGAGCTGTGTGCCACCGTCGCCAGAACCGCAAGGTGA	3000
Db	241	ACGGCTGTACTACGCGCTTCAGAGAGCTGTGTGCCACCGTCGCCAGAACCGCAAGGTGA	3000
Qy	301	GCAAGGTGGAGATTCTCCAGACGTCATTCATCATCAGGACCTTCACTTGGAGCTGA	360
Db	301	GCAAGGTGGAGATTCTCCAGACGTCATTCATCATCAGGACCTTCACTTGGAGCTGA	360
Qy	361	ACTCGGAATCCGAAGTTGGGACCCCGGGGGCCGAGAGGCTGCGCGTCCGGACTCCGCTCA	420
Db	361	ACTCGGAATCCGAAGTTGGGACCCCGGGGGCCGAGAGGCTGCGCGTCCGGACTCCGCTCA	420
Qy	421	GCAACCTTCAGCGCGACGATCAGGGCCCTGACGCGCCAGAGCGCGCATGTGTTCTTCCGACG	480
Db	421	GCAACCTTCAGCGCGACGATCAGGGCCCTGACGCGCCAGAGCGCGCATGTGTTCTTCCGACG	480
Qy	481	ATTCGATCTTTGTGTGCTGAGAGCGCTCCCGCAGGACCGCGAGACCCGACCATCAGG	540
Db	481	ATTCGATCTTTGTGTGCTGAGAGCGCTCCCGCAGGACCGCGAGACCCGACCATCAGG	540
Qy	541	GGGCAAGAGGAATTAAGTGTCTGTGTGGTTCCTCCCAAGCGCGCTTGGCGGATCTGAGG	600
Db	541	GGGCAAGAGGAATTAAGTGTCTGTGTGGTTCCTCCCAAGCGCGCTTGGCGGATCTGAGG	600
Qy	601	AGAACAAAGCCGATCGCGCGCCACTGCGCGCTTAACTGATCAGCTGCGGCTGAGGCT	660
Db	601	AGAACAAAGCCGATCGCGCGCCACTGCGCGCTTAACTGATCAGCTGCGGCTGAGGCT	660
Qy	661	GAGGCACTGGCGAGAGAGAGGGCGCTCTCTTGCAACCTACTAGTCACCAAGACTTGA	720
Db	661	GAGGCACTGGCGAGAGAGAGGGCGCTCTCTTGCAACCTACTAGTCACCAAGACTTGA	720
Qy	721	GGGGGTGGGATTCGACTCGTGTGTTCATTTTGGAAAGCAGCATTTTAAAAATGG	780
Db	721	GGGGGTGGGATTCGACTCGTGTGTTCATTTTGGAAAGCAGCATTTTAAAAATGG	780
Qy	781	TGACGTTGGTGCCTCTCGAATTTCTGAGAAATTGCTTTGATGTATATTACAATGAT	840
Db	781	TGACGTTGGTGCCTCTCGAATTTCTGAGAAATTGCTTTGATGTATATTACAATGAT	840
Qy	841	CACCGACTGAGAAATATGTTTATACATATGTTCTGTGGGGCTGTTTTTGTATTAACA	900
Db	841	CACCGACTGAGAAATATGTTTATACATATGTTCTGTGGGGCTGTTTTTGTATTAACA	900
Qy	901	AATATTAGATGTGTGAAAAAAA 926	
Db	901	AATATTAGATGTGTGAAAAAAA 926	
RESULT 2	AR206583		
LOCUS	AR206583		
DEFINITION	Sequence 3 from patent US 6372433.	DNA	linear
ACCESSION	AR206583		
VERSION	AR206583.1		
KEYWORDS	GI:21505231		
ORGANISM	Unknown.		
SOURCE	Unknown.		
REFERENCE	1 (bases 1 to 926)		
AUTHORS	Baker,B.F., Bennett,C.Frank. and Wyatt,J.		
TITLE	Antisense modulation of inhibitor of DNA binding-1 expression		
JOURNAL	Patent: US 6372433-A 3 16-Apr-2002;		
FEATURES	Location/Qualifiers		
source	1..926		

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Query Match	100.0%; Score 926; DB 6; Length 926;
Best Local Similarity	100.0%; Pred. No. 8.8e-174;

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Qy	61	CCACCGCCGCGGCGGCGCCAGCTGGCGCTGAAGCGCGGCAAGCAACGAGCGGTGGCG								120
Db	61	CCACCGCCGCGGCGGCGCCAGCTGGCGCTGAAGCGCGGCAAGCAACGAGCGGTGGCG								120
Qy	121	GGCAAGTGGTGGGCTGTCTGTCTTGAAGCAGAGCTGTGACCATTCGCGCTCCGGGCGCG								180
Db	121	GGCAAGTGGTGGGCTGTCTGTCTTGAAGCAGAGCTGTGACCATTCGCGCTCCGGGCGCG								180
Qy	181	GGGCGCGCTGCGCTGCGCTGCTGAGCAGAGCAGCAGTAAAGTGCTGTCTACGACATGA								240
Db	181	GGGCGCGCTGCGCTGCGCTGCTGAGCAGAGCAGCAGTAAAGTGCTGTCTACGACATGA								240
Qy	241	ACGGCTGTTATCTACGCGCTCAAGAGAGCTGTGTGCCACCTTGCCCAAGCGTGA								300
Db	241	ACGGCTGTTATCTACGCGCTCAAGAGAGCTGTGTGCCACCTTGCCCAAGCGTGA								300
Qy	301	GCAGAAGTGAATTCCTCCAGACCGTCAATCGACTATCATAGGAACTTCAATTGAGCTGA								360
Db	301	GCAGAAGTGAATTCCTCCAGACCGTCAATCGACTATCATAGGAACTTCAATTGAGCTGA								360
Qy	361	ATTGGAATCCGAAGTTGGAAACCCCGGGGGCCAGGAGCTGCGGCTCGGAGTCCGCTCA								420
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Qy	421	GCACCTCAAGCGGCGAATCGAGCGCCCTGACGCGCGAGGCGCATGCTTCTGCGGACG								480
Db	421	GCACCTCAAGCGGCGAATCGAGCGCCCTGACGCGCGAGGCGCATGCTTCTGCGGACG								480
Qy	481	ATCGCATTTGTGTGCTGCTGAAGCGCCTCCCCCAAGGACCGGAGCCCAAGCATCGAG								540
Db	481	ATCGCATTTGTGTGCTGCTGAAGCGCCTCCCCCAAGGACCGGAGCCCAAGCATCGAG								540
Qy	541	GGGCAAGGAATTAACGTCCTGTGGGTCTCCCCCAAGCGCGCTGCGGAGTCTGAGGG								600
Db	541	GGGCAAGGAATTAACGTCCTGTGGGTCTCCCCCAAGCGCGCTGCGGAGTCTGAGGG								600
Qy	601	AGAACAGACCCGATCGCGGCGCATGCGCCCTTAATGATTCAGCTGGGCTGAGGCT								660
Db	601	AGAACAGACCCGATCGCGGCGCATGCGCCCTTAATGATTCAGCTGGGCTGAGGCT								660
Qy	661	GAGGACCTGGGAGGAGAGGGCGCTCTCTCTGACACCTAATGATCACAGACTTTA								720
Db	661	GAGGACCTGGGAGGAGAGGGCGCTCTCTCTGACACCTAATGATCACAGACTTTA								720
Qy	721	GGGGGTGGGAATTCGACTCGTGTGTTCTAATTTTGAAGAAGCAGACATTTAAAGG								780
Db	721	GGGGGTGGGAATTCGACTCGTGTGTTCTAATTTTGAAGAAGCAGACATTTAAAGG								780
Qy	781	TGCGTTGGTGCCTTCGAGATTTCTGAGAGAAATGCTTGTATGTATTAATTAATAT								840
Db	781	TGCGTTGGTGCCTTCGAGATTTCTGAGAGAAATGCTTGTATGTATTAATTAATAT								840
Qy	841	CACCGACTGAATATTTGTTTACATATAGTCTGTGGGCTGTTTTTGTATTAACA								900
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Qy	901	AATATTTTGAATGCTGAAAAAAA 926								
Db	901	AATATTTTGAATGCTGAAAAAAA 926								

RESULT 3	AX578013	AX578013	926 bp	DNA	linear	PAT 08-JAN-2003
LOCUS	AX578013	Sequence 135 from Patent WO02081745.				
DEFINITION	AX578013					
ACCESSION	AX578013.1	GI:27647221				
VERSION						

KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
AUTHORS Garcia, T., Roman Roman, S., Baron, R., Call, K., Theilhaber, J., Connolly, T., Jackson, A., Bushnell, S.E. and Raved, G.
TITLE Genes involved in osteogenesis, and methods of use
JOURNAL Patent: WO 02081745-A 135 17-OCT-2002;
Aventis Pharma S.A. (FR)
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location/Qualifiers
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Query Match 100.0%; Score 926; DB 6; Length 926;
Best Local Similarity 100.0%; Pred. No. 8.8e-174; Mismatches 0; Indels 0; Gaps 0;
Matches 926; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGCCCATTTCTGTTTCAAGCAGTGCAGATCATGAAAGTCCGACATGCGACACCG 60
DB 1 GGGGCCCATTTCTGTTTCAAGCAGTGCAGATCATGAAAGTCCGACATGCGACACCG 60
QY 61 CCACCGCCGCGCGGCGCCCGACGCTGCGCTGAAGCGCGCAAGACAGCGAGCGGTGCGG 120
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QY 121 GCGAGATGATGCGCTGCTGCTGCTGAGAGAGCGTGGCCATCTCGGCGTGGCGGCGCGG 180
DB 121 GCGAGATGATGCGCTGCTGCTGCTGAGAGAGCGTGGCCATCTCGGCGTGGCGGCGCGG 180
QY 181 GGGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
DB 181 GGGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
QY 181 GGGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
DB 181 GGGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
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QY 421 GCACCTTCAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 480
DB 421 GCACCTTCAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 480
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DB 481 ATCGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
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DB 841 CACGACGAGATATATGTTTACATAGTCTGAGGCGGCTGTTTGTATTAACA 900
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DB 901 AATATTTAGATGTGAAAAAAA 926

RESULT 4
HSID1
LOCUS HSID1 Homo sapiens Id1 mRNA. 926 bp mRNA linear PRI 19-JAN-1995
DEFINITION X77956
ACCESSION X77956.1 GI:457784
VERSION X77956.1 GI:457784
KEYWORDS Id1 gene.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Deed, R.W., Jaslok, M. and Norton, J.D.
AUTHORS Nucleotide sequence of the cDNA encoding human helix-loop-helix Id-1 protein: identification of functionally conserved residues common to Id proteins
TITLE Biochim. Biophys. Acta 1219 (1), 160-162 (1994)
JOURNAL 94368847
MEDLINE 8086456
PUBMED 2 (bases 1 to 926)
REFERENCE Deed, R.
AUTHORS Direct Submission
TITLE Submitted (25-FEB-1994) R. Deed, Paterson Institute for Cancer Research, Dept of Regulation, Christie Hospital NHS Trust, Wilmslow Road, Manchester, UK
JOURNAL location/Qualifiers
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Query Match 100.0%; Score 926; DB 9; Length 926;
Best Local Similarity 100.0%; Pred. No. 8.8e-174; Mismatches 0; Indels 0; Gaps 0;
Matches 926; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGCCCATTTCTGTTTCAAGCAGTGCAGATCATGAAAGTCCGACATGCGACACCG 60
DB 1 GGGGCCCATTTCTGTTTCAAGCAGTGCAGATCATGAAAGTCCGACATGCGACACCG 60
QY 61 CCACCGCCGCGCGGCGCCCGACGCTGCGCTGAAGCGCGCAAGACAGCGAGCGGTGCGG 120
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Query Match      97.8%; Score 905.2; DB 9; Length 981;
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DB 95 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 154
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QY 181 GGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240
DB 215 GGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 274
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DB 275 ACGGCTGTTTACTCAGCGCTCAAGAGAGTGTGTGCTTCCACCTTGCCTCCAGAAACCGCAAGTGA 334
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QY 361 ACTCGGAATCCGAAAGTTGGAGACCCCGGGGGCGAGAGGCTGCGGTCCGGCTCCGCTCA 420
DB 395 ACTCGGAATCCGAAAGTTGGAGACCCCGGGGGCGAGAGGCTGCGGTCCGGCTCCGCTCA 454
QY 421 GCAACCTTCAAGCGCGAGATCAAGCGCCCTTGAAGCGCGAGCGCGCATGCGTCTCTGCGAGC 480
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DB 815 TCACGTTTGTGCTTCTCAGATTTCTGAGAGAAATGCTTTGATTTGATATTTACATGAT 874
QY 841 CACCGACTGAGAAATTTGTTTACAAATAGTCTGAGGGGCTGTTTTTTTGTATTAAACA 900

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DB 935 AATAATTTAGTGTGTAAGAAAAA 960

RESULT 6

LOCUS

BC012420 993 bp mRNA linear PRI 30-JUN-2004

DEFINITION Homo sapiens inhibitor of DNA binding 1, dominant negative helix-loop-helix protein, transcript variant 1, mRNA (CDNA clone MGC:9178 IMAGE:3862019), complete cds.

ACCESSION BC012420

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

1 (bases 1 to 993)

Strauberg, R.L., Felting, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shennan, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buettow, K.H., Schaefer, C.F., Bhac, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Datschenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavani, T.L., Schaefer, T.E., Brownstein, M.J., Udell, T.B., Rodlyuk, S., Carninci, P., Prange, C., Raha, S.S., Loggellano, N.A., Peters, G.J., Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Wotley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Hellon, E., Kettleman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shvachenko, Y., Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywicki, M.I., Skalska, U., Smolins, D.E., Schnerich, A., Schein, J.E., Jones, S.J., and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

2 (bases 1 to 993)

Strauberg, R.L.

Direct Submission

Submitted (15-AUG-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.ncl.nih.gov>

Contact: MGC help desk

Email: cgapbs-remail.nih.gov

Tissue Procurement: DCM/DTP

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center

Center code: BCM-HGSC

Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>

Contact: amg@bcm.tmc.edu

Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Lounsbeged, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nambavi, A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>

Series: IRAC Plate: 21 Row: 9 Column: 9.

Location/Qualifiers

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Query Match      97.8%; Score 905.2; DB 9; Length 993;
Best Local Similarity 99.4%; Pred. No. 1.2e-169;
Matches 920; Conservative 0; Mismatches 3; Indels 3; Gaps 1;

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Qy  64  CCGCCCGCCGCGCCCGCCAGTGGCGCTGAAGCGCGCAAGACAGCGAGCGGTGGCGCG 123
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Db  595  GGGGAGAGGAATTAAGTGTCTGTGGGTCGCGCCCAAGCGCGCTCGCGGATCTGAAGG 654
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RESULT 7
LOCUS      CQ726306                924 bp    DNA          linear    PAT 03-FEB-2004
DEFINITION Sequence 12240 from Patent WO02068579.
ACCESSION  CQ726306
VERSION    CQ726306.1  GI:42288983
KEYWORDS
SOURCE
ORGANISM   Homo sapiens (human)
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            Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
AUTHORS    Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
TITLE       K12s, such as nucleic acid arrays, comprising a majority of
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            thereof
JOURNAL     Patent: WO 02068579-A 12240 06-SEP-2002;
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Qy  124  AGGTGTGCGCTGCTGTCTGAGCAGAGCGGTGGCATCTCGCGCTG---CCGCGCGCGCG 180
Db  124  AGGTGTGCGCTGCTGTCTGAGCAGAGCGGTGGCATCTCGCGCTGCGCGCGCGCGCGCG 183
Qy  181  GGGCGCGCGCTGCTGCTGTGAGCAGAGCGGTGAAGAGTGAAGTGTGCTTACGACATGA 240
Db  184  GGGCGCGCGCTGCTGCTGTGAGCAGAGCGGTGAAGAGTGAAGTGTGCTTACGACATGA 243
Qy  241  ACGGCTGTACTCAAGCGCTCAAGAGAGTGGTCCGACCTGCGCCCAAGACCGCAAGGTGA 300
Db  244  ACGGCTGTACTCAAGCGCTCAAGAGAGTGGTCCGACCTGCGCCCAAGACCGCAAGGTGA 303
Qy  301  GCAAGGTGAGATTCTCCAGACGTCATCATGACTAGAGGAGCTTCAAGTTGGAGCTGA 360
Db  304  GCAAGGTGAGATTCTCCAGACGTCATCATGACTAGAGGAGCTTCAAGTTGGAGCTGA 363
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Db 364 ACTCGGAATCCGAAGTTGGAAACCCCGGGGGCCGAGGGCTGCGCGTCCGGGCTCCGCTCA 423
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Db 604 AGAACAGAACCCGATCGGCGGCACTGCGCCCTTAATCGATCCAGCTTGAGGCT 663
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Qy 781 TCAAGTTGGTCTCTCAATTTCTGAGGAAATGCTTTGATGATTAATTAATGAT 840
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Qy 901 AATAATTAGATGTGAAAA 921
Db 904 AATAATTAGATGTGTAAA 924

RESULT 8
AR206590 4793 bp DNA linear PART 20-JUN-2002
LOCUS Sequence 10 from patent US 6372433.
ACCESSION AR206590
VERSION AR206590.1 GI:21505240
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 4793)
AUTHORS Baker,B.F., Bennett,C.Frank, and Wylate,J.
TITLE Antisense modulation of inhibitor of DNA binding-1 expression
JOURNAL Patent: US 6372433-A 10 16-APR-2002;
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Best Local Similarity 78.7%; Pred. No. 1.9e-118;
Matches 913; Conservative 0; Mismatches 5; Indels 242; Gaps 2;

Qy 4 GCCCATCTGTTTCAAGCCAGTCCCAAGATCATGAAGTCCGACGTGACAGCCGCA 63
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HSU57645 4793 bp DNA linear PRI 07-FEB-1997
LOCUS Hsu57645
DEFINITION Human helix-loop-helix proteins Id-1 (ID-1) and Id-1' (ID-1') genes,
complete cde.
ACCESSION U57645
VERSION U57645.1 GI:1816511
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 4793)
Nehlin,J.O., Hara,E., Kuo,W.-L., Collins,C. and Campisi,J.
TITLE Genomic organization, sequence and chromosomal localization of the
human helix-loop-helix Id1 gene
REFERENCE 2 (bases 1 to 4793)
Nehlin,J.O., Hara,E. and Campisi,J.
AUTHORS Submitted (06-MAY-1996) Jan O. Nehlin, Cancer Biology, Lawrence
Berkeley National Laboratory, University of California, 1 Cyclotron
TITLE Direct Submision
JOURNAL Rd., Bldg. 70A-1118, Berkeley, CA 94720, USA
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Query Match 70.0%; Score 648; DB 9; Length 4793;
Best Local Similarity 78.7%; Pred. No. 1,9e-118;
Matches 913; Conservative 0; Mismatches 5; Indels 242; Gaps 2;

Qy 4 GCCCATTCGTTTTCAGCCAGTCGCAAGATCATGAAAGTCGCCAGTGGACGCCCA 63
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Db 2178 GCCCATTCGTTTTCAGCCAGTCGCAAGATCATGAAAGTCGCCAGTGGACGCCCA 2237
Qy 64 CCGCCG 123
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Qy 457 ----- 456
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Db 3018 GAACAAGACGATGCGGCGGCACTGCGCGCTTAAGTCAAGCTGCGGCTGAGGCTG 3077
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Db 3078 AGGCACTGGCAGAGAGAGGCGCTCTCTGCAACCTTCTGTGACCAAGAGACTTTAG 3137
Qy 722 GGGGTGGGATTCACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 781
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QY 842 ACCGACTGAGAAATATTGTTTACAAATAGTCTGTGGGCTGTTTGTATTAACA 901
 Db 3258 ACCGACTGAGAAATATTGTTTACAAATAGTCTGTGGGCTGTTTGTATTAACA 3317
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 Db 3318 ATTAATTAGATGGTGA AAA 3337

RESULT 10
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 AC023459 Homo sapiens chromosome 20 clone RP11-778F12 map 20, WORKING DRAFT
 DEFINITION
 AC023459 SEQUENCE, 35 unordered pieces.
 AC023459
 VERSION AC023459.2 GI:7212060
 KEYWORDS HTG; HTGS PHASE1; HTGS_DRAFT.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 1 (bases 1 to 146574)
 Birren, B., Linton, L., Nusbaum, C. and Lander, E.
 TITLE Homo sapiens chromosome 20, clone RP11-778F12
 JOURNAL Unpublished
 AUTHORS 2 (bases 1 to 146574)
 Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
 Anderson, S., Baldwin, J., Barna, N., Bida, F., Boguslavsky, L.,
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 Wu, X., Wymann, D., Ye, W. J., Young, G., Zainoun, J., Zimmer, A. and
 Zody, M.

Direct Submission
 Submitted (14-FEB-2000) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Mar 9, 2000 this sequence version replaced GI:6970679.
 All repeats were identified using RepeatMasker:
 Smit, A. F. A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR
 Web site: http://www-seq.wi.mit.edu
 Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information
 Center project name: L6806
 Center clone name: 778_F12
 ----- Summary Statistics
 Sequencing vector: M13; M7815, 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.960731
 Consensus quality: 12561 bases at least Q40
 Consensus quality: 13602 bases at least Q30
 Consensus quality: 14047 bases at least Q20
 Insert size: 15300; agarose-fp
 Insert size: 143174; sum-of-contigs
 Quality coverage: 3.1 in Q20 bases; agarose-fp
 Quality coverage: 3.3 in Q20 bases; sum-of-contigs

 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 35 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

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 2645 3875: contig of 1231 bp in length
 3876 3975: gap of 100 bp
 3976 4980: contig of 1004 bp in length
 4980 5080: gap of 100 bp
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 7861 7961: gap of 100 bp
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RESULT 11
LOCUS S78825
DEFINITION 1146 bp mRNA linear PRI 30-OCT-1995
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1146 nt].
S78825
ACCESSION S78825
VERSION S78825.1 GI:1042079
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 1146)
Zhu, W., Dahmen, J., Bulfone, A., Rigole, M., Hernandez, M.C.,
Kuo, W.L., Puelles, L., Rubenstein, V.L. and Izrael, M.A.
Id gene expression during development and molecular cloning of the
human Id-1 gene
Brain Res. Mol. Brain Res. 30 (2), 312-326 (1995)
JOURNAL 95364622
MEDLINE 7637581
PUBMED
REMARK Genbank staff at the National Library of Medicine created this
entry [NCBI gisbag 169358] from the original journal article.
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Query Match 67.3%; Score 623.2; DB 9; Length 1146;
Best Local Similarity 78.5%; Pred. No. 1.4e-113;
Matches 898; Conservative 0; Mismatches 3; Indels 243; Gaps 3;

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OY 624 CTGGGCGCTTAACTGATCCAGGCGGGGCTGAGGCTGAGGAGCTGAGGAGAGGGG 683
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OY 684 CTCTCTCTGACACCTTACTAGTACACAGACATTTAGGGGGTGGATTCACCTGCTG 743
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Db 961 TTTCTATTTTGAAGAAACAGACATTTAAAGAAATGTCAGCTGTGCTTCTAGATT 1020
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Db 1021 TCTGAGAAATTCCTTTGATTTGATTTATTAACATGATCAGGACTGAGAAATTTGTTTA 1080
OY 864 CAATAGTTC-TGTGGGGCTGTTTTTTTGTATTAACAAATTAATTAGATGTTGAAAAA 922
Db 1081 CAATAGTTCGTTGGGGCTGTTTTTTTGTATTAACAAATTAATTAGATGTTGAAAAA 1140
OY 923 AAAA 926
Db 1141 AAAA 1144

RESULT 12
LOCUS E07536
DEFINITION Human Id gene (Id-1H).
ACCESSION E07536
VERSION E07536.1 GI:2175671
KEYWORDS JP 1994141864-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 509)

AUTHORS Oda,K., Nakada,S., Hara,E., Yamaguchi,T., Nakamura,T., Oka,Y. and Kishimoto,T.
TITLE HUMAN ID GENE
JOURNAL Patent: JP 1994141864-A 1 24-MAY-1994;
SUMITOMO ELECTRIC IND LTD
OS Homo sapiens (human)
PN JP 1994141864-A/1
PD 24-MAY-1994
PF 13-NOV-1992 JP 1992328391
PI ODA KOICHIROU, NAKADA SUSUMU, HARA EIJI, YAMAGUCHI TOMOKO, PI
C12N15/12, C07H21/04, C07K13/00, C12N1/21, C12Q1/68//A61K31/70, PC
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PC C12R1.19;
CC strandedness: Double;
CC topology: Linear;
CC Feature is identified by other;
PH Key Location/Qualifiers
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FT /cell_type='TIG-1'
FT CDS 22..486
FT /product='Human Id protein'.
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Best Local Similarity 98.8%; Pred. No. 3.8e-87;
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361 GTTGGAGACCCCGGAGGCGAGAGGCTGCGGCTCGGCTCAGAACCTCAAGCGC 420
435 GAGATCAGCGCTCTGACGAGCGGAGGCGGATGCTTCTGCGAGAGATCGATCTTGT 494
421 GAGATCAGCGCTCTGACGAGCGGAGGCGGATGCTTCTGCGAGATCGATCTTGT 480
495 GCGTGAAGCGCTCCCGGAGGAGACCGGCG 524
481 GCGTGAAG-GCCTTCCCGGAGGAGACCGGCG 509

HUMID1HA
LOCUS HUMID1HA 509 bp mRNA linear PRI 14-FEB-2003
DEFINITION Homo sapiens mRNA for Id-1H, complete cds.
ACCESSION D13889
VERSION D13889.1 GI:464181
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
Hara,E., Yamaguchi,T., Nojima,H., Ide,T., Campisi,J., Okayama,H.
and Oda,K.
Id-related genes encoding helix-loop-helix proteins are required
for G1 progression and are repressed in senescent human fibroblasts
J. Biol. Chem. 269 (3), 2139-2145 (1994)
94124570
PUBMED 8294468
2 (bases 1 to 509)
REFERENCE
Hara,E.
Direct Submission
Submitted (07-DEC-1992) Eiji Hara, Science University of Tokyo,
Dept. of Biol. Science & Technol.; 2641 Yamazaki, Noda, Chiba 278,
Japan (Tel:81-471-24-1501 (ex.4421), Fax:81-471-25-1841)
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ORIGIN
Query Match 52.9%; Score 490; DB 9; Length 509;
Best Local Similarity 98.8%; Pred. No. 3.8e-87;
Matches 504; Conservative 0; Mismatches 5; Indels 1; Gaps 1;
15 TTCAGCAGTCCGCAAGATCATGAAAGTCGCCAGTGGAGACCGCCACCGCCGCG 74
1 TTCAGCAGTCCGCAAGATCATGAAAGTCGCCAGTGGAGACCGCCACCGCCGCG 60
75 GGCCTCAGTCCGCTGAGAGCCGCGCAAGACAGGAGCGGTGGGAGGTGGTGGC 134
61 GGCCTCAGTCCGCTGAGAGCCGCGCAAGACAGGAGCGGTGGGAGGTGGTGGC 120
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OM nucleic - nucleic search, using sw model

Run on: December 18, 2004, 13:49:15 ; Search time 508.452 Seconds
(without alignment)
9560.323 Million cell updates/sec

Title: US-09-996-529A-4

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	926	100.0	926	6	AA516579 DNA encod
2	926	100.0	926	6	AB234777 Coding se
3	926	100.0	926	10	ADG89363 Cancer de
4	926	100.0	926	12	ADJ75169 Marker ge
5	926	100.0	926	12	ADN04358 Antipor
6	905.2	97.8	993	12	AD124460 Human mod
7	897.2	96.9	979	5	AA544963 CDNA enco
8	893.2	96.5	1027	3	AA18245 Lung canc
9	648	70.0	4793	6	AA516586 DNA encod
10	622	67.2	1216	2	AA233520 Human pro
11	510.6	55.1	682	10	AB283034 Tox1colog
12	490	52.9	509	2	AAQ66082 Human id-
13	466	50.3	481	6	ABV78155 Human ID1
14	466	50.3	481	6	AB235731 Human ID1
15	466	50.3	481	6	ABX09974 Human ID1
16	466	50.3	481	6	AB191686 Human pol
17	447.8	48.4	483	8	AB234702 Coding se
18	443.6	47.9	958	12	ADJ77697 Human inh
19	442.2	47.8	721	2	AA40105 Gastric c
20	439.2	47.4	502	2	AAQ66083 Human id-
21	424.8	45.9	927	6	AB199635 Mouse lac

22	424.8	45.9	927	12	ADJ76041 Marker ge
23	371.8	40.2	434	10	AAK12090 Breast ca
24	343.4	37.1	1049	5	AA545151 CDNA enco
25	341.6	36.9	461	2	AA440106 Gastric c
26	289	31.2	1124	6	ABK63667 Rat seque
27	289	31.2	1124	10	ADB58118 Toxicity-
28	289	31.2	1124	10	ADB52602 Primary r
29	289	31.2	1124	12	ADP72604 Renal tox
30	283	30.6	431	3	AA69712 Human bre
31	271.4	29.3	630	6	ABT09474 Phase-1 R
32	271.4	29.3	630	10	ADG30912 Liver tox
33	271.4	29.3	630	12	ADG45499 Liver inf
34	271.4	29.3	630	12	ADH22801 Partial D
35	269	29.0	1553	6	ABQ67145 Human ang
36	268.2	29.0	1553	6	ABQ67146 Human ang
37	255.4	27.6	319	3	AA698395 Human col
38	219.4	23.7	256	6	ABK53839 Human hea
39	216.8	23.4	265	6	ABK53822 Human hea
40	210.4	22.7	217	6	ABK53894 Human hea
41	207.2	22.4	224	6	ABK53985 Human hea
42	207.2	22.4	224	6	ABK53986 Human hea
43	205.4	22.2	213	6	ABK53845 Human hea
44	199.4	21.5	201	6	ABK53900 Human hea
45	197	21.3	378	8	ABX48664 Bovine ES

ALIGNMENTS

RESULT 1	AA516579	standard; cDNA, 926 BP.
ID	AA516579;	(first entry)
AC	AA516579;	
XX		
XX		
DT	14-FEB-2002	
XX		
DE	DNA encoding human inhibitor of DNA binding-1.	
XX		
KW	Human; inhibitor of DNA binding-1; Id-1; cytostatic; antiinflammatory;	
KW	immunosuppressive; antisense therapy; antisense oligonucleotide;	
KW	hyperproliferative disorder; immune disorder; muscular disorder; ss;	
KW	vascular disorder; pancreatic disorder; infection; inflammation; tumour.	
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	CDS	36..500
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FT		/product= "Inhibitor of DNA binding-1"
PN	WO200183513-A2.	
XX		
PD	08-NOV-2001.	
XX		
PF	25-APR-2001; 2001WO-US013209.	
XX		
PR	28-APR-2000; 2000US-00561497.	
XX		
PA	(ISIS-) ISIS PHARM INC.	
XX		
PI	Baker BF, Bennett CF, Wyatt JR;	
XX		
DR	WPI, 2002-041477/05.	
XX		
DR	P-FSDB; AAU10351.	
XX		
PT	Novel antisense compound, specifically hybridizing to and inhibiting the	
FT	expression of inhibitor of DNA binding-1, useful for treating disorder.	
PT	hyperproliferative, immune, muscular, vascular or pancreatic disorder.	
PS	Example 13; Page 87-88; 105pp; English.	
XX		
CC	The invention relates to novel antisense compounds (1) 8-30 nucleobases	


```
QY 1 GGGGCCCATCTGTTTCAAGCCAGTCGCCAAGATCATGAAAGTCGCCAGTGGCAGCACCG 60
Db 1 GGGGCCCATCTGTTTCAAGCCAGTCGCCAAGATCATGAAAGTCGCCAGTGGCAGCACCG 60
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QY 901 AATAATTTAGATGTGAAAAAAA 926
Db 901 AATAATTTAGATGTGAAAAAAA 926
RESULT 3
ADG89363 standard; DNA; 926 BP.
AC ADG89363;
XX
DT 11-MAR-2004 (first entry)
XX
```

```
DE Cancer detection method related gene #26.
XX
KW ds: cancer; gene expression;
KW estrogen receptor-positive invasive breast cancer.
OS Homo sapiens.
PN W02003078662-A1.
XX
PD 25-SEP-2003.
XX
PF 12-MAR-2003; 2003WO-US007713.
XX
PR 13-MAR-2002; 2002US-0364890P.
PR 18-SEP-2002; 2002US-0412049P.
XX
PA (GENO-) GENOMIC HEALTH INC.
PI Baker JB, Cronin MT, Kiefer MC, Shak S, Walker MG;
XX
DR WPI; 2003-767536/72.
XX
PT Predicting clinical outcome for a patient diagnosed with cancer comprises
PT determining the expression level of one or more genes, and compared to
PT the amount found in a reference cancer tissue set.
XX
PS Disclosure; SEQ ID NO 311; 198bp; English.
XX
CC The invention relates to a method of predicting clinical outcome for a
CC patient diagnosed with cancer by determining the expression level of one
CC or more genes, or their expression products, selected from p53BP2,
CC cathepsin B, cathepsin L, Ki67/MIB1, and thymidine kinase in a cancer
CC tissue obtained from the patient, normalized against control gene(s), and
CC compared to the amount found in a reference cancer tissue set. The
CC specification also discloses an array comprising polynucleotides
CC hybridizing to the following genes: FOXM1, PRAME, Bcl2, STK15, CEBP1, Ki-
CC 67, GSTM1, C9, PR, BRC3, NME1, SURV, GATF3, TPRC, YB-1, DPYD, GSTJ3,
CC RPS6KB1, Sro, CHK1, ID1, BTR1, P27, CCNB1, XIAP, Chk2, CDC25B, IGF1R,
CC AKO55699, PI3KC2A, TGF3, BAG1, CYP3A4, EPCAM, VEGFC, PS2, HENT1, MISP1,
CC HNF3A, NFKBp65, BRCA2, EGFR, TKI, VDR, Contig51037, DENT1, BPHX1, IFI1A,
CC CDH1, HIF1c, IGFBP3, CTSH, Her2 and DIABLO, immobilized on a solid
CC surface. The methods are useful for predicting clinical outcome for a
CC patient diagnosed with cancer, classifying cancer, and predicting the
CC likelihood of long-term survival of a breast cancer patient, or a patient
CC diagnosed with invasive breast cancer or with estrogen receptor (ER)-
CC positive invasive breast cancer. This sequence corresponds to a gene
CC sequence whose expression is detected by the method of the invention.
XX
SQ Sequence 926 BP; 193 A; 262 C; 281 G; 190 T; 0 U; 0 Other.
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Best Local Similarity 100.0%; Pred. No. 1.5e-219;
Matches 926; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 301 GCAAGTGAAGATTCTCCAGCAGCTCATCGACTACAGGGAACCTTCAGTTGAGCTGA 360
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QY 841 CACCGACTGAGAAATTTGTTTACAAATAGTCTGTGGGGCTGTTTTTGTATTAAACA 900
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DB 901 AATAATTTAGTGTGAAAAAAA 926

RESULT 4
ADJ75169
ID ADJ75169 standard; DNA; 926 BP.
AC ADJ75169;
XX 20-MAY-2004 (first entry)
XX
DE Marker gene SEQ ID NO:421.
XX
KW bronchial asthma; chronic obstructive pulmonary disease;
KW respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;
KW gene therapy; marker gene; gene; ds.
XX
OS Homo sapiens.
XX
PN EPI394274-A2.
PD 03-MAR-2004.
XX
PF 04-AUG-2003; 2003EP-00254857.
XX
PR 06-AUG-2002; 2002JP-00229312.
XX
PR 20-MAR-2003; 2003JP-00077212.
XX
PA (GENO-) GENOX RES INC.
XX

PI Ohnani N, Sugita Y, Yamaya M, Kubo H, Nagai H, Izuwara K;
XX
XX WPI; 2004-193155/19.
XX
PT Testing for bronchial asthma or chronic obstructive pulmonary disease by
PT comparing the expression level of a marker gene in a biological sample
PT from a subject with the expression level of the gene in a sample from a
PT healthy subject.
XX
XX Claim 1; SEQ ID NO 421, 241pp; English.
XX
XX The present invention describes a method of testing for bronchial asthma
XX or chronic obstructive pulmonary disease. The method comprises
XX determining the expression level of a marker gene in a biological sample
XX from a subject, comparing the expression level determined with the
XX expression level of the marker gene in a biological sample from a healthy
XX subject, and judging whether the subject has bronchial asthma or chronic
XX obstructive pulmonary disease. The marker gene comprises: (a) a group of
XX genes (S1) whose expression levels increase when respiratory epithelial
XX cells are stimulated with interleukin-13; or (b) a group of genes (S2)
XX whose expression levels decrease when respiratory epithelial cells are
XX stimulated with interleukin-13. Also described: (1) a reagent (I) for
XX testing for bronchial asthma or chronic obstructive pulmonary disease;
XX (2) a kit for screening for a candidate compound for a therapeutic agent
XX to treat bronchial asthma or chronic obstructive pulmonary disease; (3)
XX an animal model for bronchial asthma or chronic obstructive pulmonary
XX disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a
XX method for producing an animal model for bronchial asthma or chronic
XX obstructive pulmonary disease; (6) a therapeutic agent for bronchial
XX asthma or chronic obstructive pulmonary disease, comprising the compound,
XX a marker gene or an antisense nucleic acid corresponding to a portion of
XX the marker gene, a ribozyme, a polynucleotide that suppresses the
XX expression of the gene through an RNAi effect or an antibody recognising
XX a protein encoded by a marker gene; and (7) a DNA chip for testing for
XX bronchial asthma or a chronic obstructive pulmonary disease, on which a
XX probe has been immobilised to assay a marker gene. (I) has respiratory
XX and antiasthmatic activities, and can be used in gene therapy. The method
XX is useful for testing for or screening for a therapeutic agent for
XX bronchial asthma or chronic obstructive pulmonary disease. The present
XX sequence is used in the exemplification of the present invention.
SQ Sequence 926 BP; 193 A; 262 C; 281 G; 190 T; 0 U; 0 Other;
Query Match 100.0%; Score 926; DB 12; Length 926;
Best Local Similarity 100.0%; Pred. No. 1,5e-219;
Matches 926; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGCCCATTCGTTTTCAGCCAGTCGCCAAGATCATGAAGTCGCGAGGACACCG 60
DB 1 GGGGCCCATTCGTTTTCAGCCAGTCGCCAAGATCATGAAGTCGCGAGGACACCG 60
QY 61 CCACCGCGCGCGGGGCGCCCAAGCTGCGCGCTGAAGCGCGGCAAGACAGCGAGTGGC 120
DB 61 CCACCGCGCGCGGGGCGCCCAAGCTGCGCGCTGAAGCGCGGCAAGACAGCGAGTGGC 120
QY 121 GCGAGTGTGCGCTGTCTGTGAGCAGAGCTGGGCATCTGCGTGGCGGGGCGCG 180
DB 121 GCGAGTGTGCGCTGTCTGTGAGCAGAGCTGGGCATCTGCGTGGCGGGGCGCG 180
QY 181 GGGGCGCGCTGCTGCCCTGCTGAGCAGAGCAGAGGTAACGTGTGCTTACGACATGA 240
DB 181 GGGGCGCGCTGCTGCCCTGCTGAGCAGAGCAGAGGTAACGTGTGCTTACGACATGA 240
QY 241 ACGGCTGTATCTACAGCCTTCAAGAGCTGTGCGCACCTGCGCCCGAAGACCGAAGGTGA 300
DB 241 ACGGCTGTATCTACAGCCTTCAAGAGCTGTGCGCACCTGCGCCCGAAGACCGAAGGTGA 300
QY 301 GCAAGTGAAGATTCTCCAGCAGCTCATCGACTACAGGGAACCTTCAGTTGAGCTGA 360
DB 301 GCAAGTGAAGATTCTCCAGCAGCTCATCGACTACAGGGAACCTTCAGTTGAGCTGA 360
QY 361 ACTCGAATCCGAATTGGAGCCCGGGGGCCGAGGGCTTCGGATCCGGGCTCCGCTCA 420

Db 361 ACTCGAATCCGAAATGGGAGCCCGGGGGCCGAGGCGTCCGGTCCGGCTCCGCTCA 420
QY 421 GCAACCTCAACGCGGAGATCAAGCGCCCTGACCGCCGAGGCGGACATGCGTCTCTGGGAGC 480
Db 421 GCAACCTCAACGCGGAGATCAAGCGCCCTGACCGCCGAGGCGGACATGCGTCTCTGGGAGC 480
QY 481 ATCGCATCTTGTGTGCTGAAAGCGGCTCCCGCAGGAGACCGGCGGAGCCAGCATCAAG 540
Db 481 ATCGCATCTTGTGTGCTGAAAGCGGCTCCCGCAGGAGACCGGCGGAGCCAGCATCAAG 540
QY 541 GGGCAAGAGGAATTAAGTCTGTGTGTCTCCCAACGCGCTCGCCGATCGAGG 600
Db 541 GGGCAAGAGGAATTAAGTCTGTGTGTCTCCCAACGCGCTCGCCGATCGAGG 600
QY 601 AGAACAAGACCGATGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 660
Db 601 AGAACAAGACCGATGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 660
QY 661 GAGGCACTGGGAGGAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 720
Db 661 GAGGCACTGGGAGGAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 720
QY 721 GGGGGTGGGATTCACCTGCTGTGTCTAATTTTGAAGAAGACATTTTAAAAATGG 780
Db 721 GGGGGTGGGATTCACCTGCTGTGTCTAATTTTGAAGAAGACATTTTAAAAATGG 780
QY 781 TCACGTTTGTGCTTCTCAGATTTCTGAGGAATTTGTTGTATTTAATTAATGAT 840
Db 781 TCACGTTTGTGCTTCTCAGATTTCTGAGGAATTTGTTGTATTTAATTAATGAT 840
QY 841 CACGCACTGAGAAATTTGTTTACAAATGTTCTGAGGCGTGTGTTTGTATTAACA 900
Db 841 CACGCACTGAGAAATTTGTTTACAAATGTTCTGAGGCGTGTGTTTGTATTAACA 900
QY 901 AATAATTTAGATGTGAAAAAATAA 926
Db 901 AATAATTTAGATGTGAAAAAATAA 926

RESULT 5
ID ADN04358
ADN04358 standard; cDNA; 926 BP.
XX
AC ADN04358;
XX
DT 01-JUL-2004 (first entry)
XX
DE Antipsoriatic cDNA sequence #379.
XX
KM ds; gene; antipsoriatic; gene therapy; psoriasis; diagnosis.
XX
OS Homo sapiens.
XX
PN WO2004028479-A2.
XX
PD 08-APR-2004.
XX
PF 25-SEP-2003; 2003WO-US030907.
XX
PR 25-SEP-2002; 2002US-0414006P.
XX
PA (GETH) GENENTECH INC.
XX
PI Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WI,
PI Wu TD;
XX
DR MPI; 2004-305105/28.
DR P-PSDB; ADN04359.
XX
PT New PRO nucleic acid or polypeptide, useful for preparing a
PT pharmaceutical composition for diagnosing or treating psoriasis in a
PT mammal.
XX

PS Claim 1; SEQ ID NO 752; 3069bp; English.
XX
CC The invention relates to novel polynucleotide and polypeptides for
CC treating psoriasis or a sequence having at least 80% identity to the
CC above sequences. The nucleic acid is useful for preparing a composition
CC for diagnosing or treating psoriasis in a mammal. This sequence
CC corresponds to one of the polynucleotides of the invention.
XX
SQ Sequence 926 BP; 193 A; 262 C; 281 G; 190 T; 0 U; 0 Other;
Query Match 100.0%; Score 926; DB 12; Length 926;
Best Local Similarity 100.0%; Pred. No. 1.5e-219;
Matches 926; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGCCCATTTCTGTTTCAAGCCAGTCCCAAGAAATATGAAAGTCCGCAAGTCCGACACCG 60
Db 1 GGGGCCCATTTCTGTTTCAAGCCAGTCCCAAGAAATATGAAAGTCCGCAAGTCCGACACCG 60
QY 61 CCACCG 120
Db 61 CCACCG 120
QY 121 GCGAGTGTGCGCTGTCTGTCTGAGCAGAGCGTGTGCGCATCTCGCGCTCGCGGCGCG 180
Db 121 GCGAGTGTGCGCTGTCTGTCTGAGCAGAGCGTGTGCGCATCTCGCGCTCGCGGCGCG 180
QY 181 GGGCGCGCTGCGCTGCTGCTGCTGAGCAGCAGCAGTAAAGTGTCTTACGACATGA 240
Db 181 GGGCGCGCTGCGCTGCTGCTGCTGAGCAGCAGCAGTAAAGTGTCTTACGACATGA 240
QY 241 ACGGCTGTACACAGCTCAAGAGGCTGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
Db 241 ACGGCTGTACACAGCTCAAGAGGCTGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
QY 301 GCAAGTGTGAGATTTCTCCAGCAGTCACTGATCAGGAGCCTTCAGTTGAGCTGA 360
Db 301 GCAAGTGTGAGATTTCTCCAGCAGTCACTGATCAGGAGCCTTCAGTTGAGCTGA 360
QY 361 ACTCGGAATCCGAAATTTGGGAGCCCCGGGGGCGGAGGCGTCCGGTCCGGCTCA 420
Db 361 ACTCGGAATCCGAAATTTGGGAGCCCCGGGGGCGGAGGCGTCCGGTCCGGCTCA 420
QY 421 GCAACCTCAACGCGGAGATCAAGCGCCCTGACCGGCGGCGGCGGCGGCGGCGGCG 480
Db 421 GCAACCTCAACGCGGAGATCAAGCGCCCTGACCGGCGGCGGCGGCGGCGGCGGCG 480
QY 481 ATCGCATCTTGTGTGCTGAAAGCGGCTCCCGCAGGAGACCGGCGGAGCCAGCATCAAG 540
Db 481 ATCGCATCTTGTGTGCTGAAAGCGGCTCCCGCAGGAGACCGGCGGAGCCAGCATCAAG 540
QY 541 GGGCAAGAGGAATTAAGTCTGTGTGTCTCCCAACGCGCTCGCCGATCGAGG 600
Db 541 GGGCAAGAGGAATTAAGTCTGTGTGTCTCCCAACGCGCTCGCCGATCGAGG 600
QY 601 AGAACAAGACCGATGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 660
Db 601 AGAACAAGACCGATGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 660
QY 661 GAGGCACTGGGAGGAGAGGCGGCTCTCTGCAACACTACTACTACAGAGACTTTA 720
Db 661 GAGGCACTGGGAGGAGAGGCGGCTCTCTGCAACACTACTACTACAGAGACTTTA 720
QY 721 GGGGGTGGGATTCACCTGCTGTGTCTAATTTTGAAGAAGACATTTTAAAAATGG 780
Db 721 GGGGGTGGGATTCACCTGCTGTGTCTAATTTTGAAGAAGACATTTTAAAAATGG 780
QY 781 TCACGTTTGTGCTTCTCAGATTTCTGAGGAATTTGTTGTATTTAATTAATGAT 840
Db 781 TCACGTTTGTGCTTCTCAGATTTCTGAGGAATTTGTTGTATTTAATTAATGAT 840
QY 841 CACGCACTGAGAAATTTGTTTACAAATGTTCTGAGGCGTGTGTTTGTATTAACA 900
Db 841 CACGCACTGAGAAATTTGTTTACAAATGTTCTGAGGCGTGTGTTTGTATTAACA 900

QY 901 AATATTAGATGGTGAAGAAAAA 926
Db 901 AATATTAGATGGTGAAGAAAAA 926

RESULT 6
AD124460
ID AD124460 standard; cDNA; 993 BP.
XX AD124460;
AC AD124460;
DT 15-APR-2004 (first entry)
XX
XX Human modifier of Chk1 (MCHK) encoding cDNA SEQ ID NO:10.
DE
XX Chk1 pathway modulating agent; modifier of Chk1; MCHK; cytostatic;
KM gene therapy; cancer; human; gene; ss.
XX
OS Homo sapiens.
XX
PN WO2004004785-A1.
XX
PD 15-JAN-2004.
XX
PF 09-JUL-2003; 2003WO-US021379.
XX
PR 10-JUL-2002; 2002US-039484SP.
PR 16-SEP-2002; 2002US-0410986P.
XX
XX (EXEL-) EXELIXIS INC.
XX
XX Francis-B-Iang H, Roche S, Joo DM, Nicoll M, Hal B, Zhang H;
PI Lichteig K, Amundsen CD, Jin Y, Adamkewicz JI, Platt DM;
PI Hammonds RG;
XX
DR MPI: 2004-083465/08.
DR P-PSDB; AD124510.
XX
PT Identifying a candidate Chk1 pathway modulating agent for treating e.g.,
PT cancer, comprises contacting an assay system comprising a MCHK
PT polypeptide or nucleic acid with a test agent and detecting a test agent-
PT biased activity.
XX
XX Example; SEQ ID NO 10; 266DP; English.

CC The present invention describes a method for identifying a candidate Chk1
CC pathway modulating agent. The method comprises: (a) providing an assay
CC system comprising a modifier of Chk1 (MCHK) polypeptide or nucleic acid;
CC (b) contacting the system with a test agent, where the system provides a
CC reference activity except in the presence of the test agent; and (c)
CC detecting a test agent-biased activity, and a difference between the test
CC agent-biased activity and the reference activity. Also described: (1) a
CC method for modulating Chk1 pathway of a cell; (2) a method for modulating
CC Chk1 pathway in a mammalian cell; and (3) a method for diagnosing a
CC disease in a patient. A MCHK sequence has cytostatic activity, and can be
CC used in gene therapy. The method is useful for identifying a candidate
CC Chk1 pathway-modulating agent for preparing a composition for diagnosing
CC or treating e.g., cancer. The present sequence encodes a human MCHK
CC protein, which is used in the exemplification of the present invention.
XX
XX Sequence 993 BP; 203 A; 283 C; 286 G; 221 T; 0 U; 0 Other;

Query Match 97.8%; Score 905.2; DB 12; Length 993;
Best Local Similarity 99.4%; Pred. No. 2.2e-214;
Matches 920; Conservative 0; Mismatches 3; Indels 3; Gaps 1;

QY 4 GCCCATCTGTTAGCCAGTCCGCAAGATCATGAAAGTCGCCAGTGGCAGCACCGCCA 63
Db 68 GCCCATCTGTTAGCCAGTCCGCAAGATCATGAAAGTCGCCAGTGGCAGCACCGCCA 127
QY 64 CCGCGCCGCGGCGCCAGCTGCGCTGAAGCCGCGCAGACAGAGCGAGCGGCGGCGG 123

Db 128 CCGCGCCGCGGCGCCAGCTGCGCGCTGAAGCCGCGAAGACAGCAGCGCGTCCGCG 187
QY 124 AGGTGATCGCTGCTGTCTGAGCAGAGCGCGGACATCTGCGCGT---CCGCGGCGCG 180
Db 188 AGGTGATCGCTGCTGTCTGAGCAGAGCGCGGACATCTGCGCGTCCGCGCGCGCG 247
QY 181 GCGCGCGCTGCGCTGCGCTGCGAGCAGCAGAGGTAAAGTGTCTCTCAACACATGA 240
Db 248 GCGCGCGCTGCGCTGCGCTGCGAGCAGCAGAGGTAAAGTGTCTCTCAACACATGA 307
QY 241 ACGGCTGTACTCAAGCTCAAGAGCTGTGTGCCACCTCGCCCAAGACCGAAGGTGA 300
Db 308 ACGGCTGTACTCAAGCTCAAGAGCTGTGTGCCACCTCGCCCAAGACCGAAGGTGA 367
QY 301 GCAAGGTGAGATCTCCAGCAGCTCATCATCATCATCATCATCATCATCATCATCAT 360
Db 368 GCAAGGTGAGATCTCCAGCAGCTCATCATCATCATCATCATCATCATCATCATCAT 427
QY 361 ACTCGGAATCCGAAGTTGGGACCCCGCGGCGCGAGGCGTCCGCGTCCGCTCA 420
Db 428 ACTCGGAATCCGAAGTTGGGACCCCGCGGCGCGAGGCGTCCGCGTCCGCTCA 487
QY 421 GCAACCTCAACGCGGAGATAGAGGCGCTGAGCGGCGGAGGAGGAGTCTCTCGCGAG 480
Db 488 GCAACCTCAACGCGGAGATAGAGGCGCTGAGCGGCGGAGGAGGAGTCTCTCGCGAG 547
QY 481 ATCGCATCTTGTGTGCTGAGAGCGCTCCCGCAGGACCGGCGGACCGCAGCATCAGG 540
Db 548 ATCGCATCTTGTGTGCTGAGAGCGCTCCCGCAGGACCGGCGGACCGCAGCATCAGG 607
QY 541 GGGCAAGAGGAATTTAGTGTCTGTGTGGGTCTCCCGCAAGCGGCTGCGGAGTTGA 600
Db 608 GGGCAAGAGGAATTTAGTGTCTGTGTGGGTCTCCCGCAAGCGGCTGCGGAGTTGA 667
QY 601 AGAACAAAGACCGATCGCGCGCCACTCGCGCTTAACTGCATCCAGCTGCGGCGTGA 660
Db 668 AGAACAAAGACCGATCGCGCGCCACTCGCGCTTAACTGCATCCAGCTGCGGCGTGA 727
QY 661 GAGGCACTGCGCGAGAGAGGCGGCTCTCTTGCACACCTACTAGTCACACAGACTTGA 720
Db 728 GAGGCACTGCGCGAGAGAGGCGGCTCTCTTGCACACCTACTAGTCACACAGACTTGA 787
QY 721 GGGGATGGGATTCATCGTGTGTTCTATTTTGAAGAGACATTTTAAATAATGG 780
Db 788 GGGGATGGGATTCATCGTGTGTTCTATTTTGAAGAGACATTTTAAATAATGG 847
QY 781 TCACTGTGTGTCTCTCAATTTCTGAGAAATGCTTGTATTGTATATTAATGAT 840
Db 848 TCACTGTGTGTCTCTCAATTTCTGAGAAATGCTTGTATTGTATATTAATGAT 907
QY 841 CACCGCATGGAATATTTTGTATCAATAGTTCTGTGGGCTGTTTTTGTATTAAACA 900
Db 908 CACCGCATGGAATATTTTGTATCAATAGTTCTGTGGGCTGTTTTTGTATTAAACA 967
QY 901 AATATTAGATGGTGAAGAAAAA 926
Db 968 AATATTAGATGGTGAAGAAAAA 993

RESULT 7
AAS44963
ID AAS44963 standard; cDNA; 979 BP.
XX
XX AAS44963;
AC
DT 18-DEC-2001 (first entry)
XX
XX cDNA encoding novel human secretory protein, seq ID No 44.
DE Human; secreted protein; arthritis; Crohn's disease; sepsis; shock;
KM ischaemia-reperfusion injury; haematopoiesis; cancer; neuropathy;
KM transgenic animal; Alzheimer's disease; Parkinson's disease; burn;
KM amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia;

KM ulcer; osteoporosis; bone degenerative disorder; periodontal disease;
KM gut protection; lung; liver fibrosis; immune deficiency; infection;
KM severe combined immunodeficiency; SCID; autoimmune disorder; allergy;
KM multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma;
KM fertility; analgesic; pain; antigen; ss.

OS Homo sapiens.

PN MO20016689-A2.

PD 13-SEP-2001.

PF 05-MAR-2001; 2001WO-US004942.

PR 07-MAR-2000; 2000US-00519705.

PR 19-MAY-2000; 2000US-00574454.

PR 17-JUN-2000; 2000US-00596193.

PR 14-JUL-2000; 2000US-00618847.

PR 19-SEP-2000; 2000US-00665363.

PR 20-OCT-2000; 2000US-00693267.

XX (HSE-) HSEQ INC.

XX Tang YT, Liu C, Asundi V, Xu C, Wehrman T, Ren F, Ma Y, Zhou P;

PI Zhao QA, Yang Y, Drmanac RT, Zhang J, Chen R, Xue AJ, Wang J;

XX MPI: 2001-589934/66.

XX P-PSDB; AAU28063.

XX Novel polypeptides and nucleic acids obtained from cDNA libraries

PT prepared from various human tissues, for diagnosis and treatment of

PT cancer, neurological, inflammatory, and autoimmune disorders.

XX Claim 1: SEQ ID NO 44; 107pp; English.

XX The invention relates to novel isolated human secreted polypeptides (I)

CC and polynucleotides (II). (I) and (II) are useful for treating

CC inflammatory conditions such as arthritis, nephritis, Crohn's disease,

CC ischaemia-reperfusion injury, shock, sepsis, immune responses, and is

CC involved in increasing haematopoiesis, stem cell survival, bone growth

CC and remodeling. (I), (II) and modulators of (II) are useful for

CC prophylaxis or treatment of one or more cancers. (II) is also useful for

CC creating transgenic animals useful for studying the in vivo activities of

CC the polypeptide as well as for studying modulators of the polypeptides.

CC (I) induces the proliferation of neural cells and regeneration of nerve

CC and brain tissue and is useful for the treatment of central and

CC peripheral nervous system diseases and neuropathies, such as Alzheimer's,

CC Parkinson's disease, Huntington's disease, and amyotrophic lateral

CC sclerosis. In addition, (I) is involved in chemotactic or chemokinetic

CC activity, regulation of haematopoiesis and is useful for treating myeloid

CC or lymphoid cell disorders, platelet disorders such as thrombocytopenia

CC and for regeneration of bone, cartilage, tendon, ligament and/or nerve

Sequence 979 BP; 202 A; 277 C; 283 G; 217 T; 0 U; 0 Other;

Query Match 96.9%; Score 897.2; DB 5; Length 979;

Best Local Similarity 98.8%; Pred. No. 2.1e-212;

Matches 915; Conservative 0; Mismatches 8; Indels 3; Gaps 1;

QY 4 GCCCATTCGTTTACGACGAGTCCGACGATCATGAAAGTCCGAGTGACACCGCA 63

Db 52 GCCATTCGTTTACGACGAGTCCGACGATCATGAAAGTCCGAGTGACACCGCA 111

QY 64 CCGCCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 123

Db 112 CCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 171

QY 124 AGTGTGTGCTGT 180

Db 172 AGTGTGTGCTGT 231

QY 181 GGGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240

Db 222 GGGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 291

QY 241 ACGGCTGTACTCAAGGCTCAAGGCTCAAGGCTCAAGGCTCAAGGCTCAAGGCTCA 300

Db 292 ACGGCTGTACTCAAGGCTCAAGGCTCAAGGCTCAAGGCTCAAGGCTCAAGGCTCA 351

QY 301 GCAAGTGTAGATTTCCAGCACTGATGATGATGATGATGATGATGATGATGATGAT 360

Db 352 GCAAGTGTAGATTTCCAGCACTGATGATGATGATGATGATGATGATGATGATGAT 411

QY 361 ACTGGATTCGGAATTTGGGACCCCGGGGGCGGAGGCGGCGGCGGCGGCGGCGGCGG 420

Db 412 ACTGGATTCGGAATTTGGGACCCCGGGGGCGGAGGCGGCGGCGGCGGCGGCGGCGG 471

QY 421 GCACCTTCAGCGGCGGAGATCAAGCGGCTGACGCGGCGGAGGCGGCGGCGGCGGCGG 480

Db 472 GCACCTTCAGCGGCGGAGATCAAGCGGCTGACGCGGCGGAGGCGGCGGCGGCGGCGG 531

QY 481 ATGCGATCTGT 540

Db 532 ATGCGATCTGT 591

QY 541 GGGGCAAGGAAATTAAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 600

Db 592 GGGGCAAGGAAATTAAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 651

QY 601 AGAACAAGACGATGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 660

Db 652 AGAACAAGACGATGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 711

QY 661 GAGGCACTGGGAGGAGAGGGGCGCTCTCTGTGCACTACTAGTCAACAGAGACTTGA 720

Db 712 GAGGCACTGGGAGGAGAGGGGCGCTCTCTGTGCACTACTAGTCAACAGAGACTTGA 771

QY 721 GGGGGTGGGATTCACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 780

Db 772 GGGGGTGGGATTCACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 831

QY 781 TCACGTTTGGCTCTCAGATTTCTGAGGAATTTGTTGATGTATTTATTAATGAT 840

Db 832 TCACGTTTGGCTCTCAGATTTCTGAGGAATTTGTTGATGTATTTATTAATGAT 891

QY 841 CACCGACTGAGAAATTTGTTTAAATATGTTGTGTGGGCTGTTTTTTTATTAAACA 900

Db 892 CACCGACTGAGAAATTTGTTTAAATATGTTGTGTGGGCTGTTTTTTTATTAAACA 951

QY 901 AATATTTAGATGTGAAAAAATTTT 926

Db 952 AATATTTAGATGTGAAAAAATTTT 977

RESULT 8

AAFI8245

ID AAFI8245 standard; DNA; 1027 BP.

XX AC AAFI8245;

DT	14-MAR-2001	(first entry)
XX	Lung cancer associated polynucleotide sequence SEQ ID 264.	
DB	Human; lung cancer associated protein; neuroprotective; cytosolic;	
KW	cardioactive; immunomodulatory; muscular active; vulnary;	
KW	gastrintestinal; nephrotropic; antiinfective; gynecological;	
KW	antibacterial; diagnosis; neural disorder; immune disorder; reproductive;	
KW	proliferative disorder; wound healing; infectious disease; db.	
XX	Homo sapiens.	
OS	WO20005180-A2.	
XX	21-SEP-2000.	
XX	08-MAR-2000; 2000WO-US005918.	
XX	12-MAR-1999; 99US-0124270P.	
XX	(HUMA-) HUMAN GENOME SCI INC.	
XX	(ROSE/) ROSEN C A.	
XX	Ruben SM;	
XX	WPI; 2000-587514/55.	
XX	P-PSDB; AAB58369.	
XX	Lung cancer associated gene sequences, referred to as lung cancer	
XX	antigens, useful for treatment, prevention, and diagnosis of disorders	
XX	such as lung cancer.	
XX	Claim 1; Page 724; 1425pp; English.	
XX	Polynucleotide sequences AAF17982 - AAF18424 encode human lung cancer	
XX	associated proteins represented in AAB58106 - AAB58549. Lung cancer	
XX	antagonists may have neuroprotective; cytosolic; cardioactive;	
XX	immunomodulatory; muscular active general; vulnary; gastrintestinal	
XX	general; nephrotropic; antiinfective; gynecological; or antibacterial	
XX	activity. The invention also includes antibodies specific for the protein	
XX	or polynucleotide sequences. The lung cancer associated polynucleotide	
XX	sequences may be used for detection of lung cancer, chromosome	
XX	identification, as chromosome markers, and for numerous other diagnostic	
XX	or research purposes. The proteins may be used to treat disorders such as	
XX	neural, immune, muscular, reproductive, gastrintestinal, pulmonary,	
XX	cardiovascular, renal, and proliferative disorders. The proteins may also	
XX	be used in the treatment of wounds and infectious diseases.	
XX	Polynucleotide sequences AAF18425 - AAF18433 and peptide AAB58549 are	
XX	used in the course of the invention for the identification and	
XX	characterisation of the polynucleotide and protein sequences	
XX	Sequence 1027 BP; 227 A; 287 C; 294 G; 219 T; 0 U; 0 Other;	
XX	Query Match 96.5%; Score 893.2; DB 3; Length 1027;	
XX	Best Local Similarity 99.2%; Pred. No. 2.1e-211;	
XX	Matches 919; Conservative 0; Mismatches 3; Indels 4; Gaps 2;	
QY	4 GCCCATTTGTTTCAGCCAGTCGCAAGAAATCATGAAGTGGCCAGTGGACGACGCGCA 63	
DB	74 GCCCATTTGTTTCAGCCAGTCGCAAGAAATCATGAAGTGGCCAGTGGACGACGCGCA 133	
QY	64 CCGCGCCGCGGGGCCCCAGCTGCGCGCTGAAGGCCGCGCAAGCAACGAGCGGTGCGGGCG 123	
DB	134 CCGCGCCGCGGGGCCCCAGCTGCGCGCTGAAGGCCGCGCAAGCAACGAGCGGTGCGGGCG 193	
QY	124 AGGTGTGTGCGCTGTGTGTGTGAAGCAAGCGGTGCGCATCTCGGCGTGTG---CCGCGGCGCGG 180	
DB	194 AGGTGTGTGCGCTGTGTGTGTGAAGCAAGCGGTGCGCATCTCGGCGTGTG---CCGCGGCGCGG 253	
QY	181 GGGGCGCGCTGCGCTGCGCGCGCGCAAGCAAGCAAGTAAAGTGTGCTTACGACATGGA 240	
DB	254 GGGGCGCGCTGCGCTGCGCGCGCGCAAGCAAGCAAGTAAAGTGTGCTTACGACATGGA 313	

OY	24	ACGGCTGTTATCTCAAGCCTCAAGAGAGCTGAGTCCACCTGCGCCAGAACCGCAAGGTGA	3000
Db	314	ACGGCTGTTATCTCAAGCCTCAAGAGAGCTGAGTCCACCTGCGCCAGAACCGCAAGGTGA	3727
OY	301	GCAAGGTGAGATTTCTCGACGCGTCATCGACTCATCAGAGGAACCTTCACTTTGAGCTGA	366
Db	373	GCAAGGTGAGATTTCTCGACGCGTCATCGACTCATCAGAGGAACCTTCACTTTGAGCTGA	4323
OY	361	ACTCGGAATTCGAAAGTTGGGAGACCCCGGGGGCCGAGGGCTGCGGCTCCGGCTCCGCTCA	4220
Db	433	ACTCGGAATTCGAAAGTTGGGAGACCCCGGGGGCCGAGGGCTGCGGCTCCGGCTCCGCTCA	4922
OY	421	GCAACCTCAACGGCGGAGATCAGCGCCTTGACGCGCGAGAGCGGACTGCGTTCCTGCGGACG	4880
Db	493	GCAACCTCAACGGCGGAGATCAGCGCCTTGACGCGCGAGAGCGGACTGCGTTCCTGCGGACG	5522
OY	481	ATCGCATCTTGTGTGCGCTGAGCGCTCCGCCAGGGAACGCGGACCCCAACCATCCAGG	5406
Db	553	ATCGCATCTTGTGTGCGCTGAGCGCTCCGCCAGGGAACGCGGACCCCAACCATCCAGG	6121
OY	541	GGGCGAAGAGGAATTAAGTGTCTGTGGGTCTCCGCCAAGCGGCGCTGCGCGGATCTGAGGG	6000
Db	613	GGGCGAAGAGGAATTAAGTGTCTGTGGGTCTCCGCCAAGCGGCGCTGCGCGGATCTGAGGG	6727
OY	601	AGAACAAAGACCGATCGGCGGCGACCTGCGCCTTAACTGCATCCAGCTGAGGGCTGAGGCT	6606
Db	673	AGAACAAAGACCGATCGGCGGCGACCTGCGCCTTAACTGCATCCAGCTGAGGGCTGAGGCT	7322
OY	661	GAGGCACTGGCGAGAGAGAGGGCGCTCTCTCTGCAACACTTACATGATCAAGAGACTTTA	7200
Db	733	GAGGCACTGGCGAGAGAGAGGGCGCTCTCTCTGCAACACTTACATGATCAAGAGACTTTA	7922
OY	721	GGGGGTGGGATTCACACGCTGTGTTCTAATTTTTTGAAGAACAGACATTTTAAAGAAATGG	7800
Db	793	GGGGGTGGGATTCACACGCTGTGTTCTAATTTTTTGAAGAACAGACATTTTAAAGAAATGG	8522
OY	781	TCACGTTTGGTGCTTCTCAGATTTCTGAGAAATTGCTTGTATGTATATTAACAATGAT	8406
Db	853	TCACGTTTGGTGCTTCTCAGATTTCTGAGAAATTGCTTGTATGTATATTAACAATGAT	9122
OY	841	CACCGACTGAGAAATTTGTTTAAACAATAGTCTGTGGGGCTGTTTTTTTGTATTAAACA	9000
Db	913	CACCGACTGAGAAATTTGTTTAAACAATAGTCTGTGGGGCTGTTTTTTTGTATTAAACA	9722
OY	901	AATPATTTTGAATGTGTGAAGAAAAAA 926	
Db	973	AATPATTTTGAATGTGTGAAGAAAAAA 998	
RESULT 9			
AAS16586			
ID	AAS16586 standard; cDNA; 4793 BP.		
XX	AAS16586;		
AC			
DT	14-FEB-2002 (first entry)		
XX			
DE	DNA encoding human inhibitor of DNA binding-1.		
XX			
KW	Human; inhibitor of DNA binding-1; id-1; cytosolic; antiinflammatory;		
KW	immunosuppressive; antitense therapy; antitense oligonucleotide;		
KW	hyperproliferative disorder; immune disorder; muscular disorder; ss;		
KW	vascular disorder; pancreatic disorder; infection; inflammation; tumour.		
XX			
OS	Homo sapiens.		
XX			
FH	Key		
FT	2210.2659		
FT	/tag= a		
FT	/product= "inhibitor of DNA binding-1"		
XX			
PN	WO200183513-A2.		

XX 08-NOV-2001.
PD 25-APR-2001; 2001WO-US013209.
XX 28-APR-2000; 2000US-00561497.
XX (ISIS-) ISIS PHARM INC.
XX Baker BF, Bennett CF, Wyatt JR;
PI WPI; 2002-041477/05.
DR P-PSDB; AAU10352.
XX Novel antisense compound, specifically hybridizing to and inhibiting the
PT expression of inhibitor of DNA binding-1, useful for treating
PT hyperproliferative, immune, muscular, vascular or pancreatic disorder.
XX
PS Example 15; Page 89-92; 105pp; English.
XX The invention relates to novel antisense compounds (I) 8-30 nucleobases
CC in length targeted to a nucleic acid molecule encoding inhibitor of DNA
CC binding-1, where (I) specifically hybridizes with and inhibits the
CC expression of inhibitor of DNA binding-1. Antisense inhibition of human
CC inhibitor of DNA binding-1 expression by chimeric phosphorothioate
CC oligonucleotides having 2'-methoxyethyl (2'-MOE) wings and a decoy gap
CC was tested. A series of oligonucleotides were designed to target
CC different regions of the human inhibitor of DNA binding-1 RNA. The
CC compounds were analyzed for their effect on human inhibitor of DNA
CC binding-1 mRNA levels by quantitative real-time polymerase chain reaction
CC (PCR). The result showed that the oligonucleotides showed at least 25%
CC inhibition of human inhibitor of DNA binding-1 expression. (I) is useful
CC for inhibiting the expression of inhibitor of DNA binding-1 in cells or
CC tissues by contacting the cells or tissues with (I). (I) is also useful
CC for treating a human having a disease or condition associated with
CC inhibitor of DNA binding-1 by administering a therapeutically or
CC prophylactically effective amount of (I), where the disease or condition
CC is a hyperproliferative disorder, immune disorder, muscular disorder,
CC vascular disorder or pancreatic disorder. (I) may also be used for
CC diagnostics, therapeutics, prophylaxis (e.g., to prevent or delay
CC infection, inflammation or tumor formation), and as research reagents
CC and kits. (I) may be safely and effectively administered to humans. The
CC present sequence represents the coding sequence of human inhibitor of DNA
CC binding-1, which was used to design the antisense oligonucleotides of the
CC invention.
XX
XX Sequence 4793 BP; 1038 A; 1282 C; 1339 G; 1134 T; 0 U; 0 Other;
SQ
Query Match 70.0%; Score 648; DB 6; Length 4793;
Best Local Similarity 78.7%; Pred. No. 2.8e-150;
Matches 913; Conservative 0; Mismatches 5; Indels 242; Gaps 2;
QY 4 GCCCATCTGTTTCAACGAGTCGCCAAGATCATGAAGTCGCACTGCGACGCCGCA 63
Db 2178 GCCATCTGTTTCAACGAGTCGCCAAGATCATGAAGTCGCACTGCGACGCCGCA 2237
QY 64 CCGCCGCCCGGGCCCGAGTCGCGCTGAAGCGCGCAAGACGAGCGGTGCGGGC 123
Db 2238 CCGCCGCCCGGGCCCGAGTCGCGCTGAAGCGCGCAAGACGAGCGGTGCGGGC 2297
QY 124 AGGTGTTGGCTGTCTGTCTGAGCAGAGCGTGGCCATCTCCGCGT---CCGGGGCGCG 180
Db 2298 AGGTGTTGGCTGTCTGTCTGAGCAGAGCGTGGCCATCTCCGCGTGGGGGGCGCG 2357
QY 181 GGGCGCGCTGCTGCTGCTGCTGAGCAGAGCAGGTTAAACGTGCTCTACGACATGA 240
Db 2358 GGGCGCGCTGCTGCTGCTGCTGAGCAGAGCAGGTTAAACGTGCTCTACGACATGA 2417
QY 241 ACCGCTGTTACTACGCGCTCAAGAGAGTGTCGCCACCTGCCGCCGAACCGAAGTGA 300
Db 2418 ACCGCTGTTACTACGCGCTCAAGAGAGTGTCGCCACCTGCCGCCGAACCGAAGTGA 2477
QY 301 GCAAGGTGAGATTCTCCAGCAGTCATGATCACTACAGGAGCTTCACTTGAAGTGA 360

Db 2478 GCAAGGTGAGATTCTCCAGCAGTCATGATCACTACAGGAGCTTCACTTGAAGTGA 2537
QY 361 ACTCGGAATCCGAAGTTGGAGACCCCCGGGGGCGGAGGCTGCGGATCCGGGCTCA 420
Db 2538 ACTCGGAATCCGAAGTTGGAGACCCCCGGGGGCGGAGGCTGCGGATCCGGGCTCA 2597
QY 421 GCACCTCAAGCGGCGAGATCAGCGGCTGACGCGCG----- 456
Db 2598 GCACCTCAAGCGGCGAGATCAGCGGCTGACGCGCGCGAGGTGAGATCCAGACCACT 2657
QY 457 ----- 456
Db 2658 AGATCATCTTATACCGACGGGGAACGAGGCGAGAGGGCGTGGCGCTTGACACAC 2717
QY 457 ----- 456
Db 2718 TTCCGTCCCATCTTCGCGGTACCTGCTATGCGGGGTGCTTAAGAGCCTGAAAAAG 2777
QY 457 ----- 456
Db 2778 CGCTCCCCGTCGCTCTCTGAGGAGAGGGGCGTTCCGCTGCTGCGAGCGGCTCCT 2837
QY 457 -----AGCGGCGATCGTTCTGCGAGCA 481
Db 2838 TCCAACCGCGCGTCTCATTTCTTCTCTGTTTCAAGGGGCGATGCGTCCGCGAGCA 2897
QY 482 TCGCATCTTGTGCTGCTGAGAGCGCTCCCCGAGGACCGGCGGACCCAGCCATCGAGG 541
Db 2898 TCGCATCTTGTGCTGCTGAGAGCGCTCCCCGAGGACCGGCGGACCCAGCCATCGAGG 2957
QY 542 GCGAAGAGAAATTAAGTGTCTGTGAGTGTCTCCCAAGCGCGCTGCGGATCGAGGGA 601
Db 2958 GCGAAGAGAAATTAAGTGTCTGTGAGTGTCTCCCAAGCGCGCTGCGGATCGAGGGA 3017
QY 602 GAACAAGACCGATCGCGGCGCATCGGCTTAACTGATCCAGCTGCGGCTGAGGCTG 661
Db 3018 GAACAAGACCGATCGCGGCGCATCGGCTTAACTGATCCAGCTGCGGCTGAGGCTG 3077
QY 662 AGCACTGCGGAGAGAGGGCGCTCTCTGACACACTACTAGTACCAAGACTTTAG 721
Db 3078 AGCACTGCGGAGAGAGGGCGCTCTCTGACACACTACTAGTACCAAGACTTTAG 3137
QY 722 GGGGTGGATTCACATCGTGTGTTCTATTTTAAAGACATTTTAAATGAT 781
Db 3138 GGGGTGGATTCACATCGTGTGTTCTATTTTAAAGACATTTTAAATGAT 3197
QY 782 CACGTTGGTGTCTCAGATTCTGAGAAATGCTTTGATGTTATTAATGATC 841
Db 3198 CACGTTGGTGTCTCAGATTCTGAGAAATGCTTTGATGTTATTAATGATC 3257
QY 842 ACCGACTGAGAAATTTGTTTACAATAGTCTGTGGGCGCTTTTTTGTATTAACA 901
Db 3258 ACCGACTGAGAAATTTGTTTACAATAGTCTGTGGGCGCTTTTTTGTATTAACA 3317
QY 902 ATAATTAGATGTTGAAAA 921
Db 3318 ATAATTAGATGTTGAAAA 3337
RESULT 10
AA233520
ID AA233520 standard; cDNA; 1216 BP.
XX
XX AA233520;
XX
XX 08-DEC-1999 (first entry)
XX Human prostate cancer-associated EST 44.
XX Expressed sequence tag; EST; prostate; tumor; treatment; gene therapy;
XX cancer; tissue specificity; human; ss.
XX

OS Homo sapiens.
 XX DE1981194-A1.
 XX
 XX 16-SEP-1999.
 XX
 PF 10-MAR-1998; 98DE-01011194.
 XX
 PR 10-MAR-1998; 98DE-01011194.
 XX
 PA (META-) METAGEN GES GENOMFORSCHUNG MBH.
 XX
 PI Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E, Rosenthal A;
 XX WPI, 1999-519629/44.
 DR P-PSDB; AAY48404.
 XX
 PT New nucleic acid expressed at high level in normal prostatic tissue and
 PT encoded polypeptides, used to treat cancer and screen for therapeutic
 XX agents.
 PS Claim 3; 109; 194BP, German.
 XX
 CC This invention describes novel nucleic acid sequences (A) that are
 CC expressed at high level in normal prostatic tissue. Polypeptides (I)
 CC encoded by (A) are used. (A) for identifying agents for treatment of
 CC prostatic cancer and (B) for therapy of prostate cancer, optionally where
 CC expressed by gene therapy methods. (A) is also used to isolate full-
 CC length genes (for gene therapy) and for recombinant production of (I),
 CC which can be used to raise specific antibodies. (A) are identified by
 CC assembly of ESTs (expressed sequence tags) before these are analyzed by
 CC expression pattern (tissue specificity). This approach eliminates many of
 CC the false results, as regards tissue specificity, associated with known
 CC methods that use single (usually short) ESTs. AA33477-233540 represent
 CC expressed sequence tags described in the method of the invention
 XX
 SO Sequence 1216 BP; 248 A; 349 C; 354 G; 265 T; 0 U; 0 Other;
 Query Match 67.2%; Score 622; DB 2; Length 1216;
 Best Local Similarity 77.8%; Pred. No. 4.6e-144;
 Matches 904; Conservative 0; Mismatches 15; Indels 243; Gaps 3;
 QY 4 GCCCATTTCTGTTTCAAGCAGTCCCAAGATCATGAAAGTCCAGTGGCAGCACCGGCA 63
 DB 55 GCCCATTTCTGTTTCAAGCAGTCCCAAGATCATGAAAGTCCAGTGGCAGCACCGGCA 114
 QY 64 CCG 123
 DB 115 CCG 173
 QY 124 AGGTGTCGCTGTCTGTCTGTGACAGAGCGTGGCATCTCGCGCTGCGCGCGCGCGCG 183
 DB 174 AGGTGTCGCTGTCTGTCTGTGACAGAGCGTGGCATCTCGCGCTGCGCGCGCGCGCG 230
 QY 184 CCG 243
 DB 231 GCACTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 290
 QY 244 GCTGTTACTCAAGCTTCAAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 303
 DB 291 GCTGTTACTCAAGCTTCAAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 350
 QY 304 AGGTGAGATTTCTCAAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 363
 DB 351 AGGTGAGATTTCTCAAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 410
 QY 364 CGGAATCCGAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 423
 DB 411 CGGAATCCGAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 470
 QY 424 CCTTCAACGGCGAGATCATGCGCTGACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 456
 DB 471 CCTTCAACGGCGAGATCATGCGCTGACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 530

QY 457 ----- 456
 DB 531 TCATCTTATTCACGAGCGGGGAAACGAGCGAGAGGCGTGGCGCTTGCACACATTC 590
 QY 457 ----- 456
 DB 591 CGTCCATCTTGGCGGTAACCTGGGTATGCGGGGGTGTCTTAGAGCTTGAAAAAGCGC 650
 QY 457 ----- 456
 DB 651 TCCCGCTGCTTCTTCTGAGGAAAGGGGCGCTTCTGCTGCGCTGAGCGCGCTTCTTC 710
 QY 457 -----AGGGCGCATGGCTTCTTCTGAGAGCATG 484
 DB 711 AACCGCGCGTCTATTTCTTCTGTTTTCACAGCGGCAAGCTTCTGAGCATG 770
 QY 485 CATCTTGTGTGCTGAAAGCGCTTCCCAAGGAGCCGCGGAGCCCAATCCAGGCGGCG 544
 DB 771 CATCTTGTGTGCTGAAAGCGCTTCCCAAGGAGCCGCGGAGCCCAATCCAGGCGGCG 830
 QY 545 AAGAAGATTACGTGCTCTGAGGCTTCCCGCAAGCGGCTTCCCGGATTTGAGGAGAA 604
 DB 831 AAGAAGATTACGTGCTCTGAGGCTTCCCGCAAGCGGCTTCCCGGATTTGAGGAGAA 890
 QY 605 CAATCGATTCGCGGCGCACTGCGCTTAACTGATCCAGCTGCGGCTGAGAGCTGAGG 664
 DB 891 CAATCGATTCGCGGCGCACTGCGCTTAACTGATCCAGCTGCGGCTGAGAGCTGAGG 950
 QY 665 CACTGCGAGAGAGGCGGCTCTCTCTGACACCTTACTGATGATGATGATGATGATGATG 724
 DB 951 CACTGCGAGAGAGGCGGCTCTCTCTGACACCTTACTGATGATGATGATGATGATGATG 1010
 QY 725 GTGGAATTCATCTGCTGCTGCTTATTTTGAAGAGAGATTTTAAAAATGTCAC 784
 DB 1011 GTGGAATTCATCTGCTGCTGCTTATTTTGAAGAGAGATTTTAAAAATGTCAC 1070
 QY 785 GTTGGGCTTCTCAATTTCTGAGGAATGCTTGTGATGATGATGATGATGATGATGATG 844
 DB 1071 GTTGGGCTTCTCAATTTCTGAGGAATGCTTGTGATGATGATGATGATGATGATGATG 1130
 QY 845 GACTGGAATTTATTTTCAATAGTTCGTGAGGCTGTTTTTTGTTATTAACAATA 904
 DB 1131 GACTGGAATTTATTTTCAATAGTTCGTGAGGCTGTTTTTTGTTATTAACAATA 1190
 QY 905 ATTGAGATGTAATAAAAAA 926
 DB 1191 ATTGAGATGTAATAAAAAA 1212
 RESULT 11
 ID AB283034
 AB283034 standard; cDNA; 682 BP.
 XX
 XX AB283034;
 DT 14-MAY-2003 (first entry)
 XX
 DE Toxicologically relevant human nucleotide sequence #193.
 XX
 KW Toxicologically relevant gene; toxicological response; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN W02003016500-A2.
 XX
 PD 27-FEB-2003.
 XX
 PF 16-AUG-2002; 2002WO-US026514.
 XX
 PR 16-AUG-2001; 2001US-0313080P.
 XX
 PA (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.

XX Nefc RE, Dunn RT, Adkins K, Pickett GG, Kler LD, Schmeiser K;
PI Alen P;
XX WPI; 2003-268322/26.
XX
PT Determining a toxicological response to an agent, useful for screening of
PT drugs, comprises comparing the expression profile of one or more human
PT toxic response genes to a reference gene expression profile indicative of
PT toxicity.
XX
XX Claim 1; Page 103; 455pp; English.
XX
CC The present invention describes a method (M1) for determining a
CC toxicological response to an agent, which comprises comparing the
CC expression profile of one or more human toxic response genes to a
CC reference gene expression profile indicative of toxicity, and so
CC determining the presence of a toxic response to the agent. Also
CC described: (1) an array comprising one or more polynucleotides selected
CC from the genes corresponding to the partial sequences given in AB282842
CC to AB284764, or their fragments of at least 20 nucleotides, or homologues
CC; and (2) determining if a gene putatively identified to be a toxic
CC response gene plays a role on toxic response pathways by determining the
CC expression profile of the gene after exposure of cells or a human subject
CC to a known toxic pharmaceutical or industrial agent, comprising: (a)
CC exposing cells to an agent or isolating cells from a human subject who
CC was exposed to an agent; (b) obtaining the test gene expression profile
CC for a putatively identified toxic response gene after exposure to a known
CC toxic pharmaceutical or industrial agent; and (c) comparing the test
CC profile to the expression profile of a gene with a similar function or
CC comparing the test profile to the expression profile of that gene after
CC exposure to other known toxic compounds. The methods are useful for
CC predicting and determining toxicological responses on a cellular, organ
CC or system level. The arrays comprising the human genes are useful for
CC toxicological screening of drugs, pharmaceutical compounds and chemicals
XX
SQ Sequence 682 BP; 136 A; 211 C; 212 G; 122 T; 0 U; 1 Other;
Query Match 55.1%; Score 510.6; DB 10; Length 682;
Best Local Similarity 99.2%; Pred. No. 1.6e-116;
Matches 513; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 225 CTGCTCTACGATGAGAGGGCTGTTACTACGCGCTTCAAGAGAGCTGGTCCACCCGCCC 284
DB 83 CTGCTCTACGATGAGAGGGCTGTTACTACGCGCTTCAAGAGAGCTGGTCCACCCGCCC 142
QY 285 CAGAACCGCAGAGGTGAGAGGTGAGATTCTCAGACAGCTGATGACTATCAGAGGAC 344
DB 143 CAGAACCGCAGAGGTGAGAGGTGAGATTCTCAGACAGCTGATGACTATCAGAGGAC 202
QY 345 CTTCAGTTGAGAGTGAATCTCGAATCCGAAGTTGGAGACCCCGGGGGCCGAGGGCTGCCG 404
DB 203 CTTCAGTTGAGAGTGAATCTCGAATCCGAAGTTGGAGACCCCGGGGGCCGAGGGCTGCCG 262
QY 405 GTCCGGGGCTCCGCTCAGACACCTCAACGGCGAGATAGAGGCCCTTACGCGCCGAGGGCGGA 464
DB 263 GTCCGGGGCTCCGCTCAGACACCTCAACGGCGAGATAGAGGCCCTTACGCGCCGAGGGCGGA 322
QY 465 TGCCTTCTCGCGAGAGTGCATCTTGTGTCTGCTGAGAGGCTCTCCGCCAGGAGCCGGCGG 524
DB 323 TGCCTTCTCGCGAGAGTGCATCTTGTGTCTGCTGAGAGGCTCTCCGCCAGGAGCCGGCGG 382
QY 525 ACCCCAGCCATCAAGGGGGGCAAGAGAAATTACGTGCTCTGTGGGTCTCCCCCAAGCGCGC 584
DB 383 ACCCCAGCCATCAAGGGGGGCAAGAGAAATTACGTGCTCTGTGGGTCTCCCCCAAGCGCGC 442
QY 585 TCGCCGGATCTGAGGGAGAAAGAACCGATCGGGCGGCACTGCGCCCTTAATCGATGCA 644
DB 443 TCGCCGGATCTGAGGGAGAAAGAACCGATCGGGCGGCACTGCGCCCTTAATCGATGCA 502
QY 645 GCCTGGGGCTGAGGCTGAGGCACTGGCGAGAGAGGGCGCTCTCTCTGACACCTACTA 704
DB 503 GCCTGGGGCTGAGGCTGAGGCACTGGCGAGAGAGGGCGCTCTCTCTGACACCTACTA 562

QY 705 GTACACAGAGCTTTAGGGGGTGGGATTCACACTGCG 741
DB 563 GTACACAGAGCTTTAGGGGGTGGGATTCACACTG 599
RESULT 12
AA066082
ID AA066082 standard; cDNA to mRNA; 509 BP.
XX
XX AA066082;
XX
XX 25-MAR-2003 (revised)
XX 23-JAN-1995 (first entry)
XX
XX Human Id-1H gene.
XX
XX myogenic regulatory factors; transcriptional regulatory factors;
XX diagnosis; therapy; cell proliferation; antisense therapy; de.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 22..486
XX FT /tag= a
XX FT /product= "Id-1H"
XX
XX EP60627-A1.
XX
XX 08-JUN-1994.
XX
XX 15-NOV-1993; 93EP-00309097.
XX
XX 13-NOV-1992; 92JP-00328391.
XX
XX (SUME) SUMITOMO ELECTRIC IND CO.
XX
XX Oda K, Nakada S, Hara E, Yamaguchi T, Nakamura T, Oka Y;
PI Kishimoto T;
DR WPI; 1994-177938/22.
XX
XX P-PSDB; AAR53710.
XX
XX Novel human Id genes - obtd. by probing cDNA library of human T1G-1
PT fibroblasts with synthetic oligo:nucleotide probes based on mouse Id
XX gene's conserved regions.
XX
XX
XX Claim 1; Page 10-11; 18pp; English.
XX
XX AA066082 encodes a novel human Id-1 (Id-H1). Id proteins have myogenic
CC regulatory factor activity, suppressing the activity of muscle specific
CC genes. 3 mouse Id genes have been identified and previously only Id-H2
CC (which corresponds to the mouse Id-2). The 2 human Id genes in the
CC specification are derived from the same genetic locus on a genome by
CC alternate splicing (see also AA066083 - Id-H1'). The expression of the Id
CC -H1 and Id-H1' genes specifically varies according to the state of cell
CC proliferation. In particular, the acquisition of cell aging and
CC permanently proliferating ability. The genes can be used in diagnostic
CC probes for determining the state of proliferation and state of
CC inhibition in cells. Antisense molecules may be utilised as
CC inhibitors of cell proliferation, where the Id molecules act as
CC transcriptional regulatory factors. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
SQ Sequence 509 BP; 91 A; 170 C; 172 G; 76 T; 0 U; 0 Other;
Query Match 52.9%; Score 490; DB 2; Length 509;
Best Local Similarity 98.8%; Pred. No. 1.8e-11; Indels 1; Gaps 1;
Matches 504; Conservative 0; Mismatches 5; Indels 1; Gaps 1;
QY 15 TTCACCGATGCGCCAGAGATCATGAAAGTGGCAGTGGCAGAGCCGCCCGCCGCG 74
DB 1 TTCACCGATGCGCCAGAGATCATGAAAGTGGCAGTGGCAGAGCCGCCCGCCGCG 60

QY 75 GACCCAGCAGCGCGCTGAAAGCCGCCGACAGACAGCCAGCGGTGCGAGAGTGATGCGC 13
 Db 61 GACCCACAGTCGCGCTGAAGGCGCGCAGACAGCCAGCGGTGCGAGAGTGATGCGC 12
 QY 135 TGTCTGTCTAGACAGACCGTGCATCTCGCGCTGCGAGAGCGCGAGCGCGCTGCT 19
 Db 121 TGTCTGTCTAGACAGACCGTGCATCTCGCGCTGCGAGAGCGCGAGCGCGCTGCT 18
 QY 195 GCCCTGTGAGACAGACAGCGTAAACGTGCTGCTCTACAGACATGAACGAGCTGTTACTCA 25
 Db 181 GCCCTGTGAGACAGACAGCGTAAACGTGCTGCTCTACAGACATGAACGAGCTGTTACTCA 24
 QY 255 GCGCTCAAGAGCTGTGTGCCAACCTCGGCCCAAGAACCGCAAGTGAGACGAAGTGGAAATT 31
 Db 241 GCGCTCAAGAGAGCTGTGTGCCAACCTCGGCCCAAGAACCGCAAGTGAGACGAAGTGGAAATT 30
 QY 315 CTTCAGACAGTCATGCATCACTACATCAAGGAGACCTTCAGTTGAGAGCTGAAGTCCGAATCCGAA 37
 Db 301 CTTCAGACAGTCATGCATCACTACATCAAGGAGACCTTCAGTTGAGAGCTGAAGTCCGAA 36
 QY 375 GTTGGAGACCCCGAGGGGCGGAGGGCTGCGCGGCTCCGCTCAGACCTTCACAGCGC 43
 Db 361 GTTGGAGACCCCGAGGGGCGGAGGGCTGCGCGGCTCCGCTCAGACCTTCACAGCGC 42
 QY 435 GAGATCAGCGCCCTGACCGGCGGAGCGGACATGCTCTGCGAGACGATGCGACTTGTGT 49
 Db 421 GAGATCAGCGCCCTGACCGGCGGAGCGGACATGCTCTGCGAGACGATGCGACTTGTGT 48
 QY 495 CGGTGAAGCGCTCCCGCCAGAGGACCGGCGG 52
 Db 481 CGGTGAAGCGCTCCCGCCAGAGGACCGGCGG 50

RESULT 13

ABV78155	standard; DNA; 481 BP.
ABV78155	
ABV78155;	
15-NOV-2002	(first entry)
Human ID1 DNA SEQ ID NO 39.	
RNA inhibition; dsRNA; gene expression inhibitor; oncogene; cytostatic; virucide; protozoacide; gene; ds.	
Homo sapiens.	
WO200255693-A2.	
18-JUL-2002.	
09-JAN-2002; 2002WO-EP000152.	
09-JAN-2001; 2001DE-01000586.	
26-OCT-2001; 2001DE-01055280.	
29-NOV-2001; 2001DE-01058411.	
07-DEC-2001; 2001DE-01060151.	
(RIBO-) RIBOPHARMA AG.	
Kreutzler R, Limmer S, Rost S, Hadwiger P, WPI; 2002-590671/63.	
Inhibiting expression of target gene, useful e.g. for inhibiting oncogenes, by administering double-stranded RNA complementary to the target and having an overhang.	
Claim 10; Page 135; 203pp; German.	
The invention relates to inhibiting expression of a target gene (7) by	

cell by introducing an inhibitory RNA (dsRNA1) having a double-stranded structure of at most 49 consecutive bases. At least part of one strand (a1) of dsRNA1 is complementary to (1) and at least one end of dsRNA1 has an overhang of 1-4 nucleotides. The method is used to inhibit the expression of a wide range of genes, e.g. oncogenes, cytokine genes etc. In humans, also genes in plasmidium or in viruses or viroids that are pathogenic for humans, animals or plants. Introducing an overhang into dsRNA greatly increases effectiveness for inhibiting gene expression, both in vivo and in vitro and also increases stability and thus the effective concentration inside the cell. The present sequence is that of a gene related to the invention

Query Match	50.3%	Score 466;	DB 6;	Length 481,
Best Local Similarity	100.0%;	Pred. No. 1.6e-105;		
Matches 466; Conservative	0;	Mismatches 0;	Indels 0.	Cans 0

[illegible]

RESULT 14

ID	ABZ35731 standard; DNA, 461 BP.
XX	
AC	ABZ35731,
XX	
DT	07-FEB-2003 (first entry)
DE	Human ID1 polynucleotide SEQ ID NO 39.
XX	
KW	Double stranded RNA; dsRNA; RNA; RNA inhibition; cytosolic; virucide;
KM	protozoicide; gene expression; antisense; tumour; infection; plasmodium
KV	virus; viroid; anti-GP; human; HIV; human immunodeficiency virus;
KX	Hepatitis C virus; human papilloma virus; gene; ds.
OS	Homo sapiens.
PN	DE10100588-A1.
XX	
PD	18-JUL-2002.
XX	
PP	09-JAN-2001, 2001DE-01000588.


```

QY      336 ATCAGGAGCCTTCAATTGAGGCTGAACTCGGAATCCGAAGTTGGACCCCGGGGGCCGA 395
      |||
Db      301 ATCAGGAGCCTTCAATTGAGGCTGAACTCGGAATCCGAAGTTGGACCCCGGGGGCCGA 360
QY      396 GGGCTGCCGATCCGGGCTTCGCTCAGCACCTCAACGGCGAGATCAGCGCCCTGACGGCC 455
      |||
Db      361 GGGCTGCCGATCCGGGCTTCGCTCAGCACCTCAACGGCGAGATCAGCGCCCTGACGGCC 420
QY      456 GAGCGGCGATGCGTTCCTGCGGAGCATTCGATCTTGTGTCGCTGAA 501
      |||
Db      421 GAGCGGCGATGCGTTCCTGCGGAGCATTCGATCTTGTGTCGCTGAA 466

```

Search completed: December 18, 2004, 15:33:51
 Job time : 516.452 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 18, 2004, 15:09:16 ; Search time 544.117 Seconds
(without alignments) 9395.574 Million cell updates/sec

Title: US-09-996-529A-4

Perfect score: 926

Sequence: 1 gggggccattctgttcagc.....ttgatgtgtaaaaaaaaaa 926

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4093002 seqs, 276041825 residues

Total number of hits satisfying chosen parameters: 8186004

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
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4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
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6: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
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12: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
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19: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
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21: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	926	100.0	926	US-10-388-360-311	Sequence 311, App
2	926	100.0	926	US-10-775-169-143	Sequence 143, App
3	897.2	96.9	979	US-10-291-172-44	Sequence 44, App
4	897.2	96.9	979	US-10-221-278-44	Sequence 44, App
5	897.2	96.9	1162	US-10-119-428-47	Sequence 47, App
6	893.2	96.5	1027	US-09-925-302-264	Sequence 264, App
7	893.2	96.5	1027	US-09-925-302-264	Sequence 264, App
8	466	50.3	481	US-10-384-339C-39	Sequence 39, App
9	443.6	47.9	958	US-10-453-351-1	Sequence 1, App
10	442.2	47.8	721	US-09-835-992A-30	Sequence 30, App
11	364.8	39.4	663	US-10-027-633-141641	Sequence 141641, App
12	364.8	39.4	663	US-10-027-633-141641	Sequence 141641, App

13	343.4	37.1	1049	US-10-291-172-420	Sequence 420, App
14	343.4	37.1	1049	US-10-221-278-420	Sequence 420, App
15	341.6	36.9	461	US-09-835-992A-31	Sequence 31, App
16	289	31.2	1124	US-09-917-800A-1574	Sequence 1574, App
17	289	31.2	1124	US-10-368-934-206	Sequence 206, App
18	284	30.7	326	US-10-242-535A-3578	Sequence 3578, App
19	284	30.7	326	US-10-085-783A-3578	Sequence 3578, App
20	271.4	29.3	630	US-10-404-460-92	Sequence 92, App
21	271	29.3	285	US-10-775-169-300	Sequence 300, App
22	269	29.0	1553	US-10-433-793-175	Sequence 175, App
23	268.2	29.0	1553	US-10-433-793-176	Sequence 176, App
24	255.4	27.6	319	US-09-925-299-405	Sequence 405, App
25	255.4	27.6	319	US-09-925-299-405	Sequence 405, App
26	230.4	24.9	402	US-09-833-381-1304	Sequence 1304, App
27	219.4	23.7	265	US-09-920-455-34	Sequence 34, App
28	216.8	23.4	265	US-09-920-455-17	Sequence 17, App
29	210.4	22.7	217	US-09-920-455-89	Sequence 89, App
30	207.2	22.4	224	US-09-920-455-180	Sequence 180, App
31	207.2	22.4	224	US-09-920-455-181	Sequence 181, App
32	205.4	22.2	213	US-09-920-455-40	Sequence 40, App
33	199.4	21.5	201	US-09-920-455-95	Sequence 95, App
34	197	21.3	378	US-09-960-352-13829	Sequence 13829, App
35	147	15.9	147	US-10-453-351-2	Sequence 2, App
36	142.6	15.4	556	US-10-363-345A-30861	Sequence 30861, App
37	142.6	15.4	556	US-10-363-345A-30862	Sequence 30862, App
38	135.8	14.7	556	US-10-363-345A-30863	Sequence 30863, App
39	135.8	14.7	556	US-10-363-345A-30864	Sequence 30864, App
40	112.8	12.2	556	US-10-363-345A-26981	Sequence 26981, App
41	112.8	12.2	556	US-10-363-345A-26982	Sequence 26982, App
42	111.2	12.0	556	US-10-363-345A-26983	Sequence 26983, App
43	110.6	11.9	556	US-10-363-345A-26984	Sequence 26984, App
44	110.6	11.9	2511	US-09-764-872-494	Sequence 494, App
45	107.2	11.6	530	US-09-919-580-165	Sequence 165, App

ALIGNMENTS

RESULT 1
US-10-388-360-311
; Sequence 311, Application US/10388360
; Publication No. US20030225528A1
GENERAL INFORMATION:
; APPLICANT: GENOMIC HEALTH
; APPLICANT: Baker, Joffe B.
; APPLICANT: Cronin, Maureen T.
; APPLICANT: Kiefer, Michael C.
; APPLICANT: Shaker, Steve
; APPLICANT: Walker, Michael Graham
; TITLE OF INVENTION: GENE EXPRESSION PROFILING IN BIOPSIED TUMOR TISSUES
; FILE REFERENCE: 39740-0001US
; CURRENT APPLICATION NUMBER: US/10/388,360
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 60/412,049
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: US 60/364,890
; NUMBER OF SEQ ID NOS: 384
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 311
; LENGTH: 926
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-388-360-311
Query Match 100.0% Score 926; DB 15; Length 926;
Best Local Similarity 100.0%; Pred. No. 6e-259;
Matches 926; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GGGGCCATTCTGTTCAGCCAGTGCAGATCATGTAAGTGCAGTGCAGACCG 60
DB 1 GGGGCCATTCTGTTCAGCCAGTGCAGATCATGTAAGTGCAGTGCAGACCG 60

QY	1	CCACC	CGCCGCGCGGCCCC	CACGCTCGCGCTGAAGCGCGGACAGACGACGCGTGC	120
Db	61	CCACC	CGCCGCGCGGCCCC	CACGCTCGCGCTGAAGCGCGGACAGACGACGCGTGC	120
QY	121	GCAGAGT	GTGCGCTGTCTGTCTGTAGGACGACGCGCATCTCCGCGCTGCCGGGCGCCG	180	
Db	121	GCAGAGT	GTGCGCTGTCTGTCTGTAGGACGACGCGCATCTCCGCGCTGCCGGGCGCCG	180	
QY	181	GGGCGCG	CTCGCTGCGCTGCTGTCGACGACGACGATMAAGTGTCTCTTACGACATGA	240	
Db	181	GGGCGCG	CTCGCTGCGCTGCTGTCGACGACGACGATMAAGTGTCTCTTACGACATGA	240	
QY	241	ACGCGCT	GTACTCACGCTCAAGGAGCTGTGTGCCACCTTGCCTCCAGAACCGCAAGTGA	300	
Db	241	ACGCGCT	GTACTCACGCTCAAGGAGCTGTGTGCCACCTTGCCTCCAGAACCGCAAGTGA	300	
QY	301	GCAAGT	GTGAGATCTTCCAGACGCTCATCGACTACATCAGAGACCTTCAAGTGGACCTGA	360	
Db	301	GCAAGT	GTGAGATCTTCCAGACGCTCATCGACTACATCAGAGACCTTCAAGTGGACCTGA	360	
QY	361	ACTGGA	TAATCCGAAGTTGGGACCCCGCGGGGCGGAGGGCTGCCGCTCCGCGCTCA	420	
Db	361	ACTGGA	TAATCCGAAGTTGGGACCCCGCGGGGCGGAGGGCTGCCGCTCCGCGCTCA	420	
QY	421	GCA	CCCTCAACGCGCGAGATCAGCGCCCTGAAGCGGACGAGGAGATCGGTTCTCGGAGAC	480	
Db	421	GCA	CCCTCAACGCGCGAGATCAGCGCCCTGAAGCGGACGAGGAGATCGGTTCTCGGAGAC	480	
QY	481	ATG	GCATCTTGTGTGCTGAAGCGCTCCCCAGGAGCGGCGGACCCGACGATTCGAG	540	
Db	481	ATG	GCATCTTGTGTGCTGAAGCGCTCCCCAGGAGCGGCGGACCCGACGATTCGAG	540	
QY	541	GCGCA	AGAGATTAAGTCTCTGTGGAGTCTCCCCAAGCGGCGCTCGCGGATCTGAAGG	600	
Db	541	GCGCA	AGAGATTAAGTCTCTGTGGAGTCTCCCCAAGCGGCGCTCGCGGATCTGAAGG	600	
QY	601	AAGA	CAAGACCGATCGCGCGGCACTGCGGCTTAACTGATCCAGCTGCGGCTGAGGCT	660	
Db	601	AAGA	CAAGACCGATCGCGCGGCACTGCGGCTTAACTGATCCAGCTGCGGCTGAGGCT	660	
QY	661	GAG	GCATCGGAGGAGGAGGCGCTCTCTCTGCAACCTTACTAGTCAACAGAGCTTTA	720	
Db	661	GAG	GCATCGGAGGAGGAGGCGCTCTCTCTGCAACCTTACTAGTCAACAGAGCTTTA	720	
QY	721	GCGG	GTGGATTCACCTCGTGTGTTCTATTTTGAAGAACAGACATTTAAAAAATGG	780	
Db	721	GCGG	GTGGATTCACCTCGTGTGTTCTATTTTGAAGAACAGACATTTAAAAAATGG	780	
QY	781	TCAG	CTTGGGCTTCAGATTTCTGAGGAAATGCTTTGTATGTATTAATTAATGAT	840	
Db	781	TCAG	CTTGGGCTTCAGATTTCTGAGGAAATGCTTTGTATGTATTAATTAATGAT	840	
QY	841	CAC	GACTGAGATATGTTTATACAAATGTTCTGCGGGCGTTTTTGTATTAACA	900	
Db	841	CAC	GACTGAGATATGTTTATACAAATGTTCTGCGGGCGTTTTTGTATTAACA	900	
QY	901	AATA	ATTAGATGATGAAAAAAA 926		
Db	901	AATA	ATTAGATGATGAAAAAAA 926		

RESULT 2
US-10-775-169-143
Sequence 143, Application US/10775169
Publication No. US20040175743A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Burczynski, Michael
APPLICANT: Twine, Natalie
APPLICANT: Dornier, Andrew
APPLICANT: Trepichko, William
TITLE OR INVENTION: Method for Monitoring Drug Activities In Vivo
FILE REFERENCE: AN101080 (031896-013000)

```

?
? CURRENT APPLICATION NUMBER: US/10/775,169
? CURRENT FILING DATE: 2004-02-11
? NUMBER OF SEQ ID NOS: 5278
? SOFTWARE: PatentIn version 3.2
? SEQ ID NO 143
? LENGTH: 926
? TYPE: DNA
? ORGANISM: Homo sapiens
US-10-775-169-143

Query Match      100.0%; Score 926; DB 17;
Best Local Similarity 100.0%; Pred. No. 66-259;
Matches 926; Conservative 0; Mismatches 0;

```

Query Match	Similarity	100.0%	Score 926	DB 17	Length 926
Beat Local	Similarity	100.0%	Pred. No. 6e-259		
Matches	926	Conservative	0	Mismatches	0
				Indels	0
				Gaps	0
QY	1	GGGGCCCATTTCTGTTTCAGCCAGTGCCTCCCAAGATCATGAAATGCGCATGTGCAACACG	60		
DB	1	GGGGCCCATTTCTGTTTCAGCCAGTGCCTCCCAAGATCATGAAATGCGCATGTGCAACACG	60		
QY	61	CCACCGCGCGCGGGGGCCCCAGTGTGCGCTGAGAGCGCGGCAAGACAGACGCGGTGCGG	120		
DB	61	CCACCGCGCGCGGGGGCCCCAGTGTGCGCTGAGAGCGCGGCAAGACAGACGCGGTGCGG	120		
QY	121	GCGAGGTGTGTGCGCTGTCTGTCTGAGACAGAGGTGTGCCATCTCGCGCTCCGGGGCGCG	180		
DB	121	GCGAGGTGTGTGCGCTGTCTGTCTGAGACAGAGGTGTGCCATCTCGCGCTCCGGGGCGCG	180		
QY	181	GGGGGGGGCGCTGCGCTGCTGCTGAGACAGACAGACAGATTAAGTGTGCTTACGACATGA	240		
DB	181	GGGGGGGGCGCTGCGCTGCTGCTGAGACAGACAGACAGATTAAGTGTGCTTACGACATGA	240		
QY	241	ACGGCTGTTACTCAGCGCTCAAGAGAGTGTGTGCCACCTGTGCCCAAGACCGCAAGGTGA	300		
DB	241	ACGGCTGTTACTCAGCGCTCAAGAGAGTGTGTGCCACCTGTGCCCAAGACCGCAAGGTGA	300		
QY	301	GCAAGGTGGAGATTCTCCAGACGTCATCGACTATCATGAGGACCTTCAGTTGAGCTGA	360		
DB	301	GCAAGGTGGAGATTCTCCAGACGTCATCGACTATCATGAGGACCTTCAGTTGAGCTGA	360		
QY	361	ACTCGGAATCCGAAATGGAGACCCCGGGGGGCGAGAGGGCTGCGGTGCGCGCTCCGCTCA	420		
DB	361	ACTCGGAATCCGAAATGGAGACCCCGGGGGGCGAGAGGGCTGCGGTGCGCGCTCCGCTCA	420		
QY	421	GACCCCTCAACGGCGAGATCAAGCCCTTCAAGCGCGGATGTCTTCTGCGGACG	480		
DB	421	GACCCCTCAACGGCGAGATCAAGCCCTTCAAGCGCGGATGTCTTCTGCGGACG	480		
QY	481	ATCGCATTTGTGTGCTGAAAGCGCTCCCGCAAGGACGGCGGAGACCCCAAGCCATTCAGG	540		
DB	481	ATCGCATTTGTGTGCTGAAAGCGCTCCCGCAAGGACGGCGGAGACCCCAAGCCATTCAGG	540		
QY	541	GGGGAAGGGAATTACGTGCTCTGTGGGTTCCTCCCAAGCGCGCTGCGGATCTGAGGG	600		
DB	541	GGGGAAGGGAATTACGTGCTCTGTGGGTTCCTCCCAAGCGCGCTGCGGATCTGAGGG	600		
QY	601	AGAAACAAGCCGATCGCGGCGCACTGGCGCTTAACTGATCCAGCGTGGGGCTGAGGCT	660		
DB	601	AGAAACAAGCCGATCGCGGCGCACTGGCGCTTAACTGATCCAGCGTGGGGCTGAGGCT	660		
QY	661	GAGGCATTTGCGAGAGAGAGGGCGCTCCTCTCTGCACACTTACTAGTCAACAGAGACTTGA	720		
DB	661	GAGGCATTTGCGAGAGAGAGGGCGCTCCTCTCTGCACACTTACTAGTCAACAGAGACTTGA	720		
QY	721	GGGGGTGGATTCACTCGTGTGTTCTATTTTTTGAAGAAGACATTTTAAAAATGG	780		
DB	721	GGGGGTGGATTCACTCGTGTGTTCTATTTTTTGAAGAAGACATTTTAAAAATGG	780		
QY	781	TCAAGTTGTGCTTCTCAGATTCTGAGAAATTGCTTGTATGTATATTACATGAT	840		
DB	781	TCAAGTTGTGCTTCTCAGATTCTGAGAAATTGCTTGTATGTATATTACATGAT	840		
QY	841	CACCGACTGGAATATTGTTTTTACAATAGTCTGCGGGCGTGTGTGTGTTTAAACA	900		
DB	841	CACCGACTGGAATATTGTTTTTACAATAGTCTGCGGGCGTGTGTGTGTTTAAACA	900		

QY 901 AATAATTAGATGTGAAAAA 926
Db 901 AATAATTAGATGTGAAAAA 926

RESULT 3
US-10-291-172-44
Sequence 44, Application US/10291172
Publication No. US20030228584A1
GENERAL INFORMATION:
APPLICANT: HySeq, Inc.
TITLE OF INVENTION: No. US20030228584A1 Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-045
CURRENT APPLICATION NUMBER: US/10/291,172
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: 09/693,267
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 09/665,363
PRIOR FILING DATE: 2000-09-19
PRIOR APPLICATION NUMBER: 09/616,847
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: 09/596,193
PRIOR FILING DATE: 2000-06-17
PRIOR APPLICATION NUMBER: 09/574,454
PRIOR FILING DATE: 2000-05-19
PRIOR APPLICATION NUMBER: 09/519,705
PRIOR FILING DATE: 2000-03-07
NUMBER OF SEQ ID NOS: 752
SEQ ID NO 44
LENGTH: 979
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (84)..(548)
US-10-291-172-44

Query Match 96.9%; Score 897.2; DB 15; Length 979;
Best Local Similarity 98.8%; Pred. No. 1.5e-250;
Matches 915; Conservative 0; Mismatches 8; Indels 3; Gaps 1;

QY 4 GCCCATTCGTTCTTCCAGCCAGTGCAGCAAGATCATGAAATCCCGCATGCGACACCGCA 63
Db 52 GCCCATTCGTTCTTCCAGCCAGTGCAGCAAGATCATGAAATCCCGCATGCGACACCGCA 111

QY 64 CCGCCGCGCGGGGCCAGCTCGCGCTGAAGCGCGCAAGACAGCGAGCGGTGCGGGCG 123
Db 112 CCGCCGCGCGGGGCCAGCTCGCGCTGAAGCGCGCAAGACAGCGAGCGGTGCGGGCG 171

QY 124 AGGTGTGTGCTGTCTGTCTGAGCAGAGCGTGGCCATCTCGCGCTG--CGGGGGCGCG 180
Db 172 AGGTGTGTGCTGTCTGTCTGAGCAGAGCGTGGCCATCTCGCGCTGCGCGGGGGCGCG 231

QY 181 GGGCGCGCGTGTGCTGTGCTGCTGAGCAGACAGAGTAAAGTGTGCTCTACACATGA 240
Db 232 GGGCGCGCGTGTGCTGTGCTGCTGAGCAGACAGAGTAAAGTGTGCTCTACACATGA 291

QY 241 ACGGCTGTATCTACCGCTCAAGSAGCTGTGCCCACTGTGCCCGCAGAACCGCAAGTGA 300
Db 292 ACGGCTGTATCTACCGCTCAAGSAGCTGTGCCCACTGTGCCCGCAGAACCGCAAGTGA 351

QY 301 GCAAGGTGAGATTCTTCAGCAGCTGATGACTACATCAAGGAGCCTTCAAGTTGAGCTGA 360
Db 352 GCAAGGTGAGATTCTTCAGCAGCTGATGACTACATCAAGGAGCCTTCAAGTTGAGCTGA 411

QY 361 ACTCGGAATCCGAAGTTGGAGCCCGCGGGCGCGAGGGGTGCGCGGTCCGGGCTCCGCTCA 420
Db 412 ACTCGGAATCCGAAGTTGGAGCCCGCGGGCGCGAGGGGTGCGCGGTCCGGGCTCCGCTCA 471

QY 421 GCACCTCAACGGCGGAGATCAGCGCCTTGAAGCGCGCGAGCGGCGATGCTTCCTGCGGAG 480
Db 472 GCACCTCAACGGCGGAGATCAGCGCCTTGAAGCGCGCGAGCGGCGATGCTTCCTGCGGAG 531

QY 481 ATCGCATCTGTGTGCTGAAAGCGCTCCCGCAGGAGACCGGCGAGCCCGCAGCATCCAGG 540
Db 532 ATCGCATCTGTGTGCTGAAAGCGCTCCCGCAGGAGACCGGCGAGCCCGCAGCATCCAGG 591

QY 541 GGGCAAGAGAAATTACGTGCTCTGTGGTCTCCCGCAAGCGCGCTCGCGGATCTGAGGG 600
Db 592 GGGCAAGAGAAATTACGTGCTCTGTGGTCTCCCGCAAGCGCGCTCGCGGATCTGAGGG 651

QY 601 AGAACAAACCGATGCGGCGCACTGCGCCCTTAATCTGATCAGCTGCGGCTGAGGCT 660
Db 652 AGAACAAACCGATGCGGCGCACTGCGCCCTTAATCTGATCAGCTGCGGCTGAGGCT 711

QY 661 GAGGCACTGGGAGGAGGCGGCGCTCTCTGCAACCTACTATGACCAAGACTTGA 720
Db 712 GAGGCACTGGGAGGAGGCGGCGCTCTCTGCAACCTACTATGACCAAGACTTGA 771

QY 721 GGGGCTGGGATTCACCTGCTGTGTTCTAATTTTGAAGCAGACATTTTAAAAATGG 780
Db 772 GGGGCTGGGATTCACCTGCTGTGTTCTAATTTTGAAGCAGACATTTTAAAAATGG 831

QY 781 TCACGTTGGTCTTCTCAGATTCTGAGAAATGCTTTGTATGTATTAATGAT 840
Db 832 TCACGTTGGTCTTCTCAGATTCTGAGAAATGCTTTGTATGTATTAATGAT 891

QY 841 CACGCACTGAGAAATTTGTTTACAAATGTTCTGTGGGCGCTTTTGTATTAAACA 900
Db 892 CACGCACTGAGAAATTTGTTTACAAATGTTCTGTGGGCGCTTTTGTATTAAACA 951

QY 901 AATAATTAGATGTGAAAAA 926
Db 952 AATAATTAGATGTGAAAAA 977

RESULT 4
US-10-221-278-44
Sequence 44, Application US/10221278
Publication No. US20040034208A1
GENERAL INFORMATION:
APPLICANT: HySeq, Inc.
TITLE OF INVENTION: No. US20040034208A1 Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-045
CURRENT APPLICATION NUMBER: US/10/221,278
PRIOR FILING DATE: 2002-09-06
PRIOR APPLICATION NUMBER: 09/693,267
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 09/665,363
PRIOR FILING DATE: 2000-09-19
PRIOR APPLICATION NUMBER: 09/616,847
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: 09/596,193
PRIOR FILING DATE: 2000-06-17
PRIOR APPLICATION NUMBER: 09/574,454
PRIOR FILING DATE: 2000-05-19
PRIOR APPLICATION NUMBER: 09/519,705
PRIOR FILING DATE: 2000-03-07
NUMBER OF SEQ ID NOS: 752
SEQ ID NO 44
LENGTH: 979
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (84)..(548)
US-10-221-278-44

Query Match 96.9%; Score 897.2; DB 16; Length 979;
Best Local Similarity 98.8%; Pred. No. 1.5e-250;
Matches 915; Conservative 0; Mismatches 8; Indels 3; Gaps 1;

QY 4 GCCCATTCGTTCTTCCAGCCAGTGCAGCAAGATCATGAAATCCCGCATGCGACACCGCA 63
Db 52 GCCCATTCGTTCTTCCAGCCAGTGCAGCAAGATCATGAAATCCCGCATGCGACACCGCA 111

QY	64	CCGCGCGCGCGCGCGCGCGCGCGCTGAAAGCCCGGCAAGACGCGAGCGGTGCGGCG	123
Db	112	CCGCGCGCGCGCGCGCGCGCGCGCTGAAAGCCCGGCAAGACGCGAGCGGTGCGGCG	171
QY	124	AGGTGATGCGCTGTCTGTCTGTAGAGAGCGGCGCATCTGCGCGTG---CCGGGGCGCG	180
Db	172	AGGTGATGCGCTGTCTGTCTGTAGAGAGCGGCGCATCTGCGCGTGCGCGCGCGGCGCG	231
QY	181	GGGGGCGCGCGCTGCGCGCGCTGTGAGCAGACAGCGGTAAACGTGCTCTTACACATGA	240
Db	232	GGGGGCGCGCGCTGCGCGCGCTGTGAGCAGACAGCGGTAAACGTGCTCTTACACATGA	291
QY	241	ACGGCTGTATCTACACGCTCAAGAGAGGTGAGCCACCCGCGCCAGAACCGCAAGTGA	300
Db	292	ACGGCTGTATCTACACGCTCAAGAGAGGTGAGCCACCCGCGCCAGAACCGCAAGTGA	351
QY	301	GCAAGGTGAGATTTCTTCAGACGTCATCGACTACATCAGAGACCTTCAATTGAGCTGA	360
Db	352	GCAAGGTGAGATTTCTTCAGACGTCATCGACTACATCAGAGACCTTCAATTGAGCTGA	411
QY	361	ACTCGGAATCCGAAGTTGGGACCCCGCGGGGCGGAGGCGTGCCTGCGGCTCGCTCA	420
Db	412	ACTCGGAATCCGAAGTTGGGACCCCGCGGGGCGGAGGCGTGCCTGCGGCTCGCTCA	471
QY	421	GCACTCTCAAACGCGAGATCAGCGCCCTGACGCGCCAGACGCGCATGTTCTCGGGAGAG	480
Db	472	GCACTCTCAAACGCGAGATCAGCGCCCTGAGCGCCAGACGCGCATGTTCTCGGGAGAG	531
QY	481	ATCGCATCTTGTGTGCTGTAAGCGCTCCCCCAAGGACCGCGGAGCCCGACCATCAG	540
Db	532	ATCGCATCTTGTGTGCTGTAAGCGCTCCCCCAAGGAGCGCGGAGCCCGACCATCAG	591
QY	541	GCGCAAGAGAAATTACGTCTCTGTGGGTCTCCCCAAGCGCGCTGCGCGATCTGAGGG	600
Db	592	GCGCAAGAGAAATTACGTCTCTGTGGGTCTCCCCAAGCGCGCTGCGCGATCTGAGGG	651
QY	601	AAGAACAAACCGATGCGCGGCCACTGCGCTTAACTGCATCAGCTGGGCTGAGGCT	660
Db	652	AAGAACAAACCGATGCGCGGCCACTGCGCTTAACTGCATCAGCTGGGCTGAGGCT	711
QY	661	GAGGCACTGCGCAGAGAGAGGGGCTCTCTCTGCAACACTATATATACACAGACTTGA	720
Db	712	GAGGCACTGCGCAGAGAGAGGGGCTCTCTCTGCAACACTATATATACACAGACTTGA	771
QY	721	GGGGGTGGGATTCACCTGCTGTGTTTCAATTTTGAAGAAGCAGCATTTTAAAAATGG	780
Db	772	GGGGGTGGGATTCACCTGCTGTGTTTCAATTTTGAAGAAGCAGCATTTTAAAAATGG	831
QY	781	TCAAGTTGGGTCTCTCAGATTTCTGAGAAATTTGCTTTGATTTGATATTAATCATGAT	840
Db	832	TCAAGTTGGGTCTCTCAGATTTCTGAGAAATTTGCTTTGATTTGATATTAATCATGAT	891
QY	841	CACCGACTGAGAAATTTGTTTACAAATAGTCTGAGGGGCTGTTTTTGTATTTAAACA	900
Db	892	CACCGACTGAGAAATTTGTTTACAAATAGTCTGAGGGGCTGTTTTTGTATTTAAACA	951
QY	901	AATAATTAGATGTGTAAGAAAAA 926	
Db	952	AATAATTAGATGTGTAAGAAAAA 977	

```

: APPLICANT: Ma, Yundong
: APPLICANT: Zhou, ping
: APPLICANT: Zhao, Qing A.
: APPLICANT: Yang, Yonghong
: APPLICANT: Dimañac, Radoje T.
: TITLE OF INVENTION: No. US20030165881A1el Nucleic Acids and
: TITLE OF INVENTION: Polypeptides
: FILE REFERENCE: 789CIP2
: CURRENT APPLICATION NUMBER: US/10/119,428
: CURRENT FILING DATE: 2002-04-09
: PRIOR APPLICATION NUMBER: 09/596,193
: PRIOR FILING DATE: 2000-06-17
: PRIOR APPLICATION NUMBER: 09/574,454
: PRIOR FILING DATE: 2000-05-19
: PRIOR APPLICATION NUMBER: 09/519,705
: PRIOR FILING DATE: 2000-03-07
: NUMBER OF SEQ ID NOS: 55
: SOFTWARE: pc_FL_genes Version 1.0
: SEQ ID NO 47
: LENGTH: 1162
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (267)..(734)
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (1)....(1162)
: OTHER INFORMATION: n = a,c,t,c or g
US-10-119-428-47

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RESULT 5
US-10-119-428-47
Sequence 47, Application US/10119428
Publication No. US20030165881A1
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Xu, Chongjun
APPLICANT: Wehman, Tom
APPLICANT: Ren, Feiyen

Query Match	Similarity	96.9%	Score	897.21	DB	15	Length	1162
Best Local	Similarity	98.8%	Pred.	No.1.7e-250				
Matches	915	Conservative	0	Mismatches	8	Indels	3	Gaps
QY	4	GCCCATTTCTGTTTCAGCCAGTCGCGCAGAAATCATGAAAGTCGCGAGTGGACGACCCGCCA	63					
Db	235	GCCCATTTCTGTTTCAGCCAGTCGCGCAGAAATCATGAAAGTCGCGAGTGGACGACCCGCCA	294					
QY	64	CCGCGCGCCGCGGGGCCCGCAGCTGCGCCGCTTGAAAGCCGGCAGACAGCGAGCGGTGCGGCG	123					
Db	295	CCGCGCGCCGCGGGGCCCGCAGCTGCGCCGCTTGAAAGCCGGCAGACAGCGAGCGGTGCGGCG	354					
QY	124	AGGTGTGTGCGCTGTCTGTCTGTAGACAGACGCTGACATCTCGCGCTG---CCGGGGGCGCG	180					
Db	355	AGGTGTGTGCGCTGTCTGTCTGTAGACAGACGCTGACATCTCGCGCTGCGCGCGGGGCGCG	414					
QY	181	GGGGCGCCGCTGCTCGCCGCGCTGTGGAACAAGCAGCAGAGTAAACGTGCTGCTTACGACATGA	240					
Db	415	GGGGCGCCGCTGCTCGCCGCGCTGTGGAACAAGCAGCAGAGTAAACGTGCTGCTTACGACATGA	474					
QY	241	ACGGCTGTACTACAGCCTCAAGAGAGCTGTGCCCCACCTCGCCCAAGAACCGAGAGGTGA	300					
Db	475	ACGGCTGTACTACAGCCTCAAGAGAGCTGTGCCCCACCTCGCCCAAGAACCGAGAGGTGA	534					
QY	301	GCAAGGTGGAGATTCTCCAGACAGTCAATGCACTAACACAGGAACTTTCAAGTTGAACTGA	360					
Db	535	GCAAGGTGGAGATTCTCCAGACAGTCAATGCACTAACACAGGAACTTTCAAGTTGAACTGA	594					
QY	361	ACTCGGAATCGAAGTTGGACCCCCCGGGGGCGAGAGGCTGCGGGTCCGGGGCTCCGCTCA	420					
Db	595	ACTCGGAATCGAAGTTGGAAACCCCGGGGGCGAGAGGCTGCGGGTCCGGGGCTCCGCTCA	654					
QY	421	GCAACCTCAACGGCGAGATCAAGGCGCTCTGAACGCGCAGAGGGGCGATCGTTCTTGCGAGAC	480					
Db	655	GCAACCTCAACGGCGAGATCAAGGCGCTCTGAACGCGCAGAGGGGCGATCGTTCTTGCGAGAC	714					
QY	481	ATGCAATCTGTGTGCTGTAAGCGCTTCCCGAGGGAACGGGCGGAACTCCAGCGCATCCAG	540					
Db	715	ATGCAATCTGTGTGCTGTAAGCGCTTCCCGAGGGAACGGGCGGAACTCCAGCGCATCCAG	774					
QY	541	GGGCAAGAGGAATTACGTGCTCTGTGTGGTCTTCCCCAACGCGCTTGCAGGATTTGAGG	600					

Db 775 GGGCAAGAGAAATTAAGTGTCTGTGGTCTCCCAAGCGCTCGCCGATCTGAGGG 834
Qy 601 AGAAGAAAGCCGATGGGGGGCCATGCGCCCTTAATCTGATCCAGCTGGGGCTGAGGCT 660
Db 835 AGAAGAAAGCCGATGGGGGGCCATGCGCCCTTAATCTGATCCAGCTGGGGCTGAGGCT 894
Qy 661 GAGGACTGGGAGGAGGAGGGGCTCTCTGCAACCTACTAGTCAAGAGACTTTA 720
Db 895 GAGGACTGGGAGGAGGAGGGGCTCTCTGCAACCTACTAGTCAAGAGACTTTA 954
Qy 721 GGGGGTGGGATTCACCTCGTGTGTCTAATTTTGAAGAGACATTTTAAAAATGG 780
Db 955 GGGGGTGGGATTCACCTCGTGTGTCTAATTTTGAAGAGACATTTTAAAAATGG 1014
Qy 781 TCACCTTTGGTCTCTCAGATTTCTGAGGAAATGCTTTGTATTGTAATTAATGAT 840
Db 1015 TCACCTTTGGTCTCTCAGATTTCTGAGGAAATGCTTTGTATTGTAATTAATGAT 1074
Qy 841 CACCGACTGAGAAATTTGTTTACAATAGTCTGAGGGCTGTTTTTTGTTAATAACA 900
Db 1075 CCCCCAGTGAATAATTTGTTTACAATAGTCTGAGGGCTGTTTTTTGTTAATAACA 1134
Qy 901 AATAATTTAGATGTGTGAAAAA 926
Db 1135 AATAATTTAGATGTGTGAAAAA 1160

RESULT 6

US-09-925-302-264
; Sequence 264, Application US/09925302
; Patent No. US20020044941A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 264
; LENGTH: 1027
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-302-264

Query Match 96.5%; Score 893.2; DB 9; Length 1027;
Best Local Similarity 99.2%; Pred. No. 2.3e-249;
Matches 919; Conservative 0; Mismatches 3; Indels 4; Gaps 2;
Qy 4 GCCCATTCGTTTCAGCCAGTGGCCCAAGATCATGAAGTCCGACGTGCGACACCGCA 63
Db 74 GCCCATTCGTTTCAGCCAGTGGCCCAAGATCATGAAGTCCGACGTGCGACACCGCA 133
Qy 64 CCGCGCGCCGCGGAGCCCACTGCGCTGAAGGCGCGCAAGACAGCGAGTGGCGGCG 123
Db 134 CCGCGCGCGCGGAGCCCACTGCGCTGAAGGCGCGCAAGACAGCGAGTGGCGGCG 193
Qy 124 AGGTGGTGGCTGTGTCTGTGACAGAGCGTGGCCATCTCGCGCTG--CCGCGGCGCG 180
Db 194 AGGTGGTGGCTGTGTCTGTGACAGAGCGTGGCCATCTCGCGCTGCGCGGCGCGCG 253
Qy 181 GGGCGCGCGCTGCTGCTGCTGAGAGACAGAGAGTAAAGTGTGCTCTGACATGA 240
Db 254 GGGCGCGCGCTGCTGCTGCTGAGAGACAGAGAGTAAAGTGTGCTCTGACATGA 313
Qy 241 ACGGCTGTACTACACGCTCAAGAGAGTGTGCGCCACCTGCGCCAGAACCGCAAGTGA 300
Db 314 ACGGCTGTACTACACGCTCAAGAGAGTGTGCGCCACCTGCGCCAGAACCGCAAGTGA 372

Qy 301 GCAAGTGGAGATTCTCCAGACGTCATCGATCATCAGGAGACCTTTCAGTTGAGCTGA 360
Db 373 GCAAGTGGAGATTCTCCAGACGTCATCGATCATCAGGAGACCTTTCAGTTGAGCTGA 432
Qy 361 ACTGGAAATCCGAAGTTGGAGCCCCCGGGGCGGAGGCGCTGCCGCTCCGCTCA 420
Db 433 ACTGGAAATCCGAAGTTGGAGCCCCCGGGGCGGAGGCGCTGCCGCTCCGCTCA 492
Qy 421 GCACCTCTAAGGGGAGATTCAGGCGCTGAGGCGCGAGGCGAGCATGCGTTCTCGGGAG 480
Db 493 GCACCTCTAAGGGGAGATTCAGGCGCTGAGGCGCGAGGCGAGCATGCGTTCTCGGGAG 552
Qy 481 ATCGCATCTGTGTCTGTAAGCGCTCCCGCAGGGAACCGGCGAGCCCGACATCCAG 540
Db 553 ATCGCATCTGTGTGTCTGTAAGCGCTCCCGCAGGGAACCGGCGAGCCCGACATCCAG 612
Qy 541 GGGCAAGAGAAATTCGTCCTGTGTGTCTCTCCCGAAGCGGCTGCGGATCTGAGGG 600
Db 613 GGGCAAGAGAAATTCGTCCTGTGTGTCTCTCCCGAAGCGGCTGCGGATCTGAGGG 672
Qy 601 AGAAGAAAGCCGATGGGCGGCACTGCGCCCTTAATCTGATCCAGCTGGGGCTGAGGCT 660
Db 673 AGAAGAAAGCCGATGGGCGGCACTGCGCCCTTAATCTGATCCAGCTGGGGCTGAGGCT 732
Qy 661 GAGGCACTGGGAGGAGGAGGCGCTCTCTCTGCAACCTACTAGTCAACAGACTTTA 720
Db 733 GAGGCACTGGGAGGAGGAGGCGCTCTCTCTGCAACCTACTAGTCAACAGACTTTA 792
Qy 721 GGGGGTGGGATTCACCTCGTGTGTCTAATTTTGAAGAGACATTTTAAAAATGG 780
Db 793 GGGGGTGGGATTCACCTCGTGTGTCTAATTTTGAAGAGACATTTTAAAAATGG 852
Qy 781 TCACCTTTGGTCTCTCAGATTTCTGAGGAAATGCTTTGTATTGTAATTAATGAT 840
Db 853 TCACCTTTGGTCTCTCAGATTTCTGAGGAAATGCTTTGTATTGTAATTAATGAT 912
Qy 841 CACCGACTGAGAAATTTGTTTACAATAGTCTGAGGGCTGTTTTTTGTTAATAACA 900
Db 913 CACCGACTGAGAAATTTGTTTACAATAGTCTGAGGGCTGTTTTTTGTTAATAACA 972
Qy 901 AATAATTTAGATGTGTGAAAAA 926
Db 973 AATAATTTAGATGTGTGAAAAA 998

RESULT 7

US-09-925-302-264
; Sequence 264, Application US/09925302
; Patent No. US20030064072A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 264
; LENGTH: 1027
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-302-264

Query Match 96.5%; Score 893.2; DB 10; Length 1027;
Best Local Similarity 99.2%; Pred. No. 2.3e-249;
Matches 919; Conservative 0; Mismatches 3; Indels 4; Gaps 2;
Qy 4 GCCCATTCGTTTCAGCCAGTGGCCCAAGATCATGAAGTCCGACGTGCGACACCGCA 63


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; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 1
; LENGTH: 958
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: probe for Id1
US-10-453-351-1

Query Match      47.9%; Score 443.6; DB 16; Length 958;
Best Local Similarity 95.5%; Pred. No. 2,3e-118;
Matches 468; Conservative 0; Mismatches 19; Indels 3; Gaps 1;

QY      4  GCCCATTTCTTTTTCAGCCAGTCGCCAAGATCATAAAGTGGCCAGTGGCAGCACCGCA 63
DB      31  GCCCATTTCTTTTTCAGCCAGTCGCCAAGATCATAAAGTGGCCAGTGGCAGCACCGCA 90
QY      64  CCGCCGCGCGGGGCCCCAGCTGCGGCTGAAGGCGGCAAGACAGCGAGCGGTGCGGCG 123
DB      91  CCGCCGCGCGGGGCCCCAGCTGCGGCTGAAGGCGGCAAGACAGCGAGCGGTGCGGCG 150
QY     124  AGGTGTGCGCTGTCTGTCTGAGCAGAGCGTGGCCATCTCGGCGTG---CCGGGGCGCG 180
DB     151  AGGTGTGCGCTGTCTGTCTGAGCAGAGCGTGGCCATCTCGGCGTGCGCGCGGGGCGCG 210
QY     181  GGGGCGCGCTGCTGCTGCTGAGCAGAGCGTAAAGTGTGCTGCTTAACGACATGA 240
DB     211  GGGGCGCGCTGCTGCTGCTGAGCAGAGCGTAAAGTGTGCTGCTTAACGACATGA 270
QY     241  ACGGCTGTACTCAGCGCTCAAGGAGCTGTGCCACCGTGGCCAGAACGCGAAGTGA 300
DB     271  ACGGCTGTACTCAGCGCTCAAGGAGCTGTGCCACCGTGGCCAGAACGCGAAGTGA 330
QY     301  GCAAGGTGAGATTTCTCCAGCAGCATCATCATCAGGAGACCTTCAGTTGAGCTGA 360
DB     331  GCAAGGTGAGATTTCTCCAGCAGCATCATCATCAGGAGACCTTCAGTTGAGCTGA 390
QY     361  ACTCGGAATCCGAAGTTGGAAACCCCGGGGGCCGAGGGCTGCGGGTCCGCTCA 420
DB     391  ACTCGGAATCCGAAGTTGGAAACCCCGGGGGCCGAGGGCTGCGGGTCCGCTCA 450
QY     421  GCACCTCAAGGGGAGATCAGCGGCTGAGCGGCGGAGGCGGAGCGCTTCCTGCGAG 480
DB     451  GCACCTCAAGGGGAGATCAGCGGCTGAGCGGCGGAGGCGGAGCGCTTCCTGCGAG 510
QY     481  ATCGCATCTT 490
DB     511  AGATCATCTT 520

RESULT 10
US-09-835-992A-30
; Sequence 30, Application US/09835992A
; Patent No. US20020037541A1
; GENERAL INFORMATION:
; APPLICANT: Obata, Yuichi
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES ASSOCIATED WITH GASTRIC CANCER AN
; FILE REFERENCE: 10461/7112
; CURRENT APPLICATION NUMBER: US/09/835,992A
; CURRENT FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: US 08/896,164
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 30
; LENGTH: 721
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: Unsure
; LOCATION: (264)..(264)
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; OTHER INFORMATION: n = a, c, g or t
; NAME/KEY: Unsure
; LOCATION: (488)..(488)
; OTHER INFORMATION: n = a, c, g or t
; NAME/KEY: Unsure
; LOCATION: (512)..(512)
; OTHER INFORMATION: n = a, c, g or t
; NAME/KEY: Unsure
; LOCATION: (538)..(538)
; OTHER INFORMATION: n = a, c, g or t
; NAME/KEY: Unsure
; LOCATION: (548)..(548)
; OTHER INFORMATION: n = a, c, g or t
; NAME/KEY: Unsure
; LOCATION: (605)..(605)
; OTHER INFORMATION: n = a, c, g or t
; NAME/KEY: Unsure
; LOCATION: (611)..(611)
; OTHER INFORMATION: n = a, c, g or t
; NAME/KEY: Unsure
; LOCATION: (660)..(660)
; OTHER INFORMATION: n = a, c, g or t
; NAME/KEY: Unsure
; LOCATION: (669)..(669)
; OTHER INFORMATION: n = a, c, g or t
US-09-835-992A-30

Query Match      47.8%; Score 442.2; DB 9; Length 721;
Best Local Similarity 95.1%; Pred. No. 5e-118;
Matches 466; Conservative 0; Mismatches 21; Indels 3; Gaps 1;

QY      4  GCCCATTTCTTTTTCAGCCAGTCGCCAAGATCATAAAGTGGCCAGTGGCAGCACCGCA 63
DB      31  GCCCATTTCTTTTTCAGCCAGTCGCCAAGATCATAAAGTGGCCAGTGGCAGCACCGCA 90
QY      64  CCGCCGCGCGGGGCCCCAGCTGCGGCTGAAGGCGGCAAGACAGCGAGCGGTGCGGCG 123
DB      91  CCGCCGCGCGGGGCCCCAGCTGCGGCTGAAGGCGGCAAGACAGCGAGCGGTGCGGCG 150
QY     124  AGGTGTGCGCTGTCTGTCTGAGCAGAGCGTGGCCATCTCGGCGTG---CCGGGGCGCG 180
DB     151  AGGTGTGCGCTGTCTGTCTGAGCAGAGCGTGGCCATCTCGGCGTGCGCGGGGCGCG 210
QY     181  GGGGCGCGCTGCTGCTGCTGAGCAGAGCGTAAAGTGTGCTGCTTAACGACATGA 240
DB     211  GGGGCGCGCTGCTGCTGCTGAGCAGAGCGTAAAGTGTGCTGCTTAACGACATGA 270
QY     241  ACGGCTGTACTCAGCGCTCAAGGAGCTGTGCCACCGTGGCCAGAACGCGAAGTGA 300
DB     271  ACGGCTGTACTCAGCGCTCAAGGAGCTGTGCCACCGTGGCCAGAACGCGAAGTGA 330
QY     301  GCAAGGTGAGATTTCTCCAGCAGCATCATCATCAGGAGACCTTCAGTTGAGCTGA 360
DB     331  GCAAGGTGAGATTTCTCCAGCAGCATCATCATCAGGAGACCTTCAGTTGAGCTGA 390
QY     361  ACTCGGAATCCGAAGTTGGAAACCCCGGGGGCCGAGGGCTGCGGGTCCGCTCA 420
DB     391  ACTCGGAATCCGAAGTTGGAAACCCCGGGGGCCGAGGGCTGCGGGTCCGCTCA 450
QY     421  GCACCTCAAGGGGAGATCAGCGGCTGAGCGGCGGAGGCGGAGCGCTTCCTGCGAG 480
DB     451  GCACCTCAAGGGGAGATCAGCGGCTGAGCGGCGGAGGCGGAGCGCTTCCTGCGAG 510
QY     481  ATCGCATCTT 490
DB     511  AMATCATCTT 520
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RESULT 11
US-10-027-632-141641
; Sequence 141641, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
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/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
/ POLYMORPHISMS IN THE HUMAN GENOME
/ FILE REFERENCE: 108827.129
/ CURRENT APPLICATION NUMBER: US/10/027,632
/ PRIOR FILING DATE: 2002-04-30
/ PRIOR APPLICATION NUMBER: US 60/218,006
/ PRIOR FILING DATE: 2000-07-12
/ PRIOR APPLICATION NUMBER: US 60/198,676
/ PRIOR FILING DATE: 2000-04-20
/ PRIOR APPLICATION NUMBER: US 60/193,483
/ PRIOR FILING DATE: 2000-03-29
/ PRIOR APPLICATION NUMBER: US 60/185,218
/ PRIOR FILING DATE: 2000-02-24
/ PRIOR APPLICATION NUMBER: US 60/167,363
/ PRIOR FILING DATE: 1999-11-23
/ PRIOR APPLICATION NUMBER: US 60/156,358
/ PRIOR FILING DATE: 1999-09-28
/ PRIOR APPLICATION NUMBER: US 60/146,002
/ PRIOR FILING DATE: 1999-08-09
/ NUMBER OF SEQ ID NOS: 325720
/ SOFTWARE: FASTSEQ for Windows Version 4.0
/ SEQ ID NO 141641
/ LENGTH: 663
/ TYPE: DNA
/ ORGANISM: Human
US-10-027-632-141641

Query Match      39.4%; Score 364.8; DB 13; Length 663;
Best Local Similarity 94.6%; Pred. No. 1.7e-95;
Matches 388; Conservative 1; Mismatches 18; Indels 3; Gaps 1;

QY      84 TGGCGCTGAAAGCCCGCAAGACAGCGGTGCGGCGAGGTGCTGCTGCT 143
DB      1 TGGCGCTGAAAGCCCGCAAGACAGCGGTGCGGCGAGGTGCTGCTGCT 60
QY     144 GAGCAGAGCTGTCATCTCGCGCTG---CCGGGGCGCGGGCGCGCTGCTGCT 200
DB      61 GAGCAGAGCTGTCATCTCGCGCTG---CCGGGGCGCGGGCGCGCTGCTGCT 120
QY     201 CTGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 260
DB     121 CTGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 180
QY     261 AAGAGCTGTGCTCCACCTGCTCCACGACGACGACGACGACGACGACGACGAC 320
DB     181 AAGAGCTGTGCTCCACCTGCTCCACGACGACGACGACGACGACGACGACGAC 240
QY     321 CACGTCATGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 380
DB     241 CACGTCATGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 300
QY     381 ACCCGCGGGGCGGAGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGG 440
DB     301 ACCCGCGGGGCGGAGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGG 360
QY     441 AGCGCCCTGACGCGCGGAGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 490
DB     361 AGCGCCCTGACGCGCGGAGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 410

RESULT 12
US-10-027-632-141641
/ Sequence 141641, Application US/10027632
/ Publication No. US20030204075A9
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
/ POLYMORPHISMS IN THE HUMAN GENOME
/ FILE REFERENCE: 108827.129
/ CURRENT APPLICATION NUMBER: US/10/027,632
/ PRIOR FILING DATE: 2002-04-30
/ PRIOR APPLICATION NUMBER: US 60/218,006
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/ PRIOR FILING DATE: 2000-07-12
/ PRIOR APPLICATION NUMBER: US 60/198,676
/ PRIOR FILING DATE: 2000-04-20
/ PRIOR APPLICATION NUMBER: US 60/193,483
/ PRIOR FILING DATE: 2000-03-29
/ PRIOR APPLICATION NUMBER: US 60/185,218
/ PRIOR FILING DATE: 2000-02-24
/ PRIOR APPLICATION NUMBER: US 60/167,363
/ PRIOR FILING DATE: 1999-11-23
/ PRIOR APPLICATION NUMBER: US 60/156,358
/ PRIOR FILING DATE: 1999-09-28
/ PRIOR APPLICATION NUMBER: US 60/146,002
/ PRIOR FILING DATE: 1999-08-09
/ NUMBER OF SEQ ID NOS: 325720
/ SOFTWARE: FASTSEQ for Windows Version 4.0
/ SEQ ID NO 141641
/ LENGTH: 663
/ TYPE: DNA
/ ORGANISM: Human
US-10-027-632-141641

Query Match      39.4%; Score 364.8; DB 15; Length 663;
Best Local Similarity 94.6%; Pred. No. 1.7e-95;
Matches 388; Conservative 1; Mismatches 18; Indels 3; Gaps 1;

QY      84 TGGCGCTGAAAGCCCGCAAGACAGCGGTGCGGCGAGGTGCTGCTGCT 143
DB      1 TGGCGCTGAAAGCCCGCAAGACAGCGGTGCGGCGAGGTGCTGCTGCT 60
QY     144 GAGCAGAGCTGTCATCTCGCGCTG---CCGGGGCGCGGGCGCGCTGCTGCT 200
DB      61 GAGCAGAGCTGTCATCTCGCGCTG---CCGGGGCGCGGGCGCGCTGCTGCT 120
QY     201 CTGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 260
DB     121 CTGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 180
QY     261 AAGAGCTGTGCTCCACCTGCTCCACGACGACGACGACGACGACGACGACGAC 320
DB     181 AAGAGCTGTGCTCCACCTGCTCCACGACGACGACGACGACGACGACGACGAC 240
QY     321 CACGTCATGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 380
DB     241 CACGTCATGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 300
QY     381 ACCCGCGGGGCGGAGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGG 440
DB     301 ACCCGCGGGGCGGAGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGG 360
QY     441 AGCGCCCTGACGCGCGGAGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 490
DB     361 AGCGCCCTGACGCGCGGAGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 410

RESULT 13
US-10-291-172-420
/ Sequence 420, Application US/10291172
/ Publication No. US20030228584A1
/ GENERAL INFORMATION:
/ APPLICANT: HySeq, Inc
/ TITLE OF INVENTION: No. US20030228584A1 Nucleic Acids and Polypeptides
/ FILE REFERENCE: 21272-045
/ CURRENT APPLICATION NUMBER: US/10/291,172
/ PRIOR FILING DATE: 2000-11-08
/ PRIOR APPLICATION NUMBER: 09/693,267
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 09/665,363
/ PRIOR FILING DATE: 2000-09-19
/ PRIOR APPLICATION NUMBER: 09/616,847
/ PRIOR FILING DATE: 2000-07-14
/ PRIOR APPLICATION NUMBER: 09/596,193
/ PRIOR FILING DATE: 2000-06-17
/ PRIOR APPLICATION NUMBER: 09/574,454
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/ PRIOR FILING DATE: 2000-05-19
/ PRIOR APPLICATION NUMBER: 09/519,705
/ PRIOR FILING DATE: 2000-03-07
/ NUMBER OF SEQ ID NOS: 752
/ SEQ ID NO: 420
/ LENGTH: 1049
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-291-172-420

Query Match 37.1%; Score 343.4; DB 15; Length 1049;
Best Local Similarity 74.7%; Pred. No. 3.7e-89;
Matches 742; Conservative 0; Mismatches 181; Indels 70; Gaps 22;

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QY 4 GCCCATTTCTGTTTCCAGTCGCGCAAGATCATGAAGTCCCGCATGGCAGCACCGGCA 63
DB 55 GCCCATTTCTGTTTCCAGTCGCGCAAGATCATGAAGTCCCGCATGGCAGCACCGGCA 114
QY 64 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 122
DB 115 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 174
QY 123 GAGGTGTGCGCTGTGTGT-CTGACGACGCGTGCAT-----CTGCGCGTGCAGG 175
DB 175 GAGGTGTGCGCTGTGTGTGACGACGCGTGCATTTCTGCGGTGCGCGCGCGCG 234
QY 176 CGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 233
DB 235 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 294
QY 234 GACA-TGAAGGCGTGT-ACTCAGCGCTCAAGAGCTGTGCGCGCGCGCGCGCGCGCGCG 287
DB 295 GACATTGAAGCGCTGTTAACCTACGCGCTCAAGAGCTGTGCGCGCGCGCGCGCGCG 354
QY 288 AACCGCAAGGTGAGCAAGGTGAGATTCTCCAGCAGTCACT-----GACTACATC 338
DB 355 CCCGCAAGGTGAGCAAGGTGAGATTCTCCAGCAGTCACTTCACTTACATTACAG 414
QY 339 AGGACCTTCAAGTTGAGCTGAA---CTCGAATTCGAAAGTTGGGACCCCGCGCGCG 394
DB 415 GGACCTTTCAGTTGGAGCTGAACTTCGCGAATCCGAAAGTTGGGACCCCGCGCGCG 474
QY 395 AGGCGTGCAGGCTCCGCGCTCCGCTC-----AGCACTCCCAAGCGCGAGAT--CAGCGCC 446
DB 475 CGAGGCGCTCCGCGGCTCCGCGCTCCGCTCAAGCAGCTTCAAGCGCGAGATTCAAGCGCC 534
QY 447 CTGACGCGCGAGG--CGGATCGTGTCTGCGGAGATCGATCTTGTGTCTGCTGAAGCG 504
DB 535 CTGACGCGCGAGGCGGCGCATGCTTCTGCGGAGATCGATCTTGTGTCTGCTGAAGCG 594
QY 505 CTTCCCTCCAGGAGCGGCGGAGCCCAAGCATCA-----GGGCGCGAAGAGATTAC 556
DB 595 CTTCCCTCCAGGAGCGGCGGAGCCCAAGCATCA-----GGGCGCGAAGAGATTAC 654
QY 557 GTGCTCTGTGGTCT-----CCCCCAAGCGGCTCCCGCGAGTGTGAGAG--AGAAACAG 608
DB 655 CGTGCTCTGTGGTCTTTCCTCCCAAGCGGCTCCCGCGAGTGTGAGAGAAACAAGC 714
QY 609 ACCGATCGGCGGCGCATGCGCGCTTAA-----CTGATCGAGCTGGGCGTGAAGCTGAGG 664
DB 715 CGAATCGGCGGCGCATGCGCGCTTAAAGCTGAGTCCACGCTGGGCGTGAAGCTGAGG 774
QY 665 CACTGCGGAGAGAGGCGGCTCTCTCTGAC--ACCTAATGTCACAGAGACTTTTAAAG 722
DB 775 CACTGCGGAGAGAGGCGGCTCTCTCTGACCACTTCTTGTGACAGAGACTTTTAAAG 834
QY 723 GGGGGGAGTT--CCACTGCTGTGTCTTATTTT--GAAAGCAGAGATTTTAAAG 779
DB 835 GGGGGGAGTTCCCACTGCTGTGTCTTATTTT--GAAAGCAGAGATTTTAAAG 894
QY 780 GTCAAGTTGTGTCTTCTAGATTTCTGAGAAATTC--TTGTATTTGATATTTACAT 837
DB 895 GTCAAGTTGTGTCTTCTAGATTTCTGAGAAATTCGATTTATGATATTTACAT 954
```

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QY 838 GATCA-CCGACTGAGAAATATTTTACATAGTTC--TGTGGGCGTGTGTGTGTA 893
DB 955 GATCACCGCACTGAAAAAATGTTTACAAATAGTCTTGTGGGTGTTTTTGTGAT 1014
QY 894 TTAACCAATATTTAGATGTTGAAAAA 926
DB 1015 TTAACCAATATTTAGATGTTGAAAAA 1047
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RESULT 14
US-10-221-278-420
Sequence 420, Application US/10221278
Publication No. US20040034208A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc
TITLE OF INVENTION: No. US20040034208A1el Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-045
CURRENT APPLICATION NUMBER: US/10/221,278
CURRENT FILING DATE: 2002-09-06
PRIOR APPLICATION NUMBER: 09/693,267
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 09/665,363
PRIOR FILING DATE: 2000-09-19
PRIOR APPLICATION NUMBER: 09/616,847
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: 09/596,193
PRIOR FILING DATE: 2000-06-17
PRIOR APPLICATION NUMBER: 09/574,454
PRIOR FILING DATE: 2000-05-19
PRIOR APPLICATION NUMBER: 09/519,705
PRIOR FILING DATE: 2000-03-07
NUMBER OF SEQ ID NOS: 752
SEQ ID NO: 420
LENGTH: 1049
TYPE: DNA
ORGANISM: Homo sapiens
US-10-221-278-420

Query Match 37.1%; Score 343.4; DB 16; Length 1049;
Best Local Similarity 74.7%; Pred. No. 3.7e-89;
Matches 742; Conservative 0; Mismatches 181; Indels 70; Gaps 22;

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QY 4 GCCCATTTCTGTTTCCAGTCGCGCAAGATCATGAAGTCCCGCATGGCAGCACCGGCA 63
DB 55 GCCCATTTCTGTTTCCAGTCGCGCAAGATCATGAAGTCCCGCATGGCAGCACCGGCA 114
QY 64 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 122
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QY 339 AGGACCTTCAAGTTGAGCTGAA---CTCGAATTCGAAAGTTGGGACCCCGCGCGCG 394
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QY 395 AGGCGTGCAGGCTCCGCGCTCCGCTC-----AGCACTCCCAAGCGCGAGAT--CAGCGCC 446
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Db 1015 TTAACCAATATTATTAGATGTGAAAAAAA 1047

RESULT 15
US-09-996-529a-31/c
Sequence 31, Application US/09835992A
Patent No. US20020037541A1
GENERAL INFORMATION:
APPLICANT: Obata, Yuichi
TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES ASSOCIATED WITH GASTRIC CANCER AND
METHODS FOR DIAGNOSING AND TREATING GASTRIC CANCER
FILE REFERENCE: L0461/7112
CURRENT APPLICATION NUMBER: US/09/835,992A
CURRENT FILING DATE: 2001-04-16
PRIOR APPLICATION NUMBER: US 08/896,164
PRIOR FILING DATE: 1997-07-17
NUMBER OF SEQ ID NOS: 87
SOFTWARE: Patent version 3.0
SEQ ID NO 31
LENGTH: 461
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Best Local Similarity 79.3%: Pred. No. 8.1e-89;
Matches 365; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

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QY 517 ACCGCGGACCCCAAGCCATCCAGGGGCGAAGAGAAATTAAGTCTCTGTGGGTCTCCCC 576
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QY 577 AACCGCTCGCCGAGTCTGAGGAGAAACAAGCCGAGCGGCACTGGCCCTTAAC 636
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    |||||
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    |||||
DB 281 TGNATNCAGCCTGGGGNTGNGAGTGAAGCAATGNGNGAGAGNGGNTNCTTTTGAN 222
    |||||
QY 697 ACTTACTAGTCACCAAGACCTTTAAGGGGTGGATTCACCTGTTGTCTATTTTGG 756
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DB 221 ACTTAAATGTAACCAAGAAATTTAAGGGGTGGANTNCAATTGNGNTTTTAAATTTTG 162
    |||||
QY 757 AAAAGCAGACATTTTAAAAAATGTCACGTTTGTGCTTCACATTTCTGAGAAATG 816
    |||||
DB 161 NAAAGCAGAAATTTTAAAAAATGTTNAGNTTGTGNTTTNAGAAATTTTNGGGAANTG 102
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    |||||
DB 101 NTTGTATTTGANAATACNANGATNACCGAATGAAATATTTGTTTACNATAGTTTGTG 42
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QY 877 GGGCTGTTTTTTTGTATTTAAACAATATTTAATGTTG 916
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DB 41 GGGNTGTTTTTTTGTATTTAANNAATTAATTAAGTGTG 2
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Search completed: December 18, 2004, 20:42:43
Job time : 549.117 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 18, 2004, 15:00:58 ; Search time 3370.83 Seconds
(without alignments)
10010.347 Million cell updates/sec

Title: US-09-996-529a-4

Perfect score: 1 gggggccattctcttccagc.....ttagatggtgataaaaaaa 926

Sequence: 1 gggggccattctcttccagc.....ttagatggtgataaaaaaa 926

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues
Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

1: gb_eest1:*
2: gb_eest2:*
3: gb_hic:*
4: gb_eest3:*
5: gb_eest4:*
6: gb_eest5:*
7: gb_eest6:*
8: gb_gsest1:*
9: gb_gsest2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	897	96.9	950	3	CR591965 full-length
2	897	96.9	952	3	CR615862 full-length
3	897	96.9	970	3	CR599901 full-length
4	895.2	96.7	958	3	CR621997 full-length
5	887.4	95.8	951	1	AL546878 full-length
6	866.2	93.5	938	3	CR600217 full-length
7	844.4	91.2	938	5	CR610338 full-length
8	844	91.1	868	3	CR610338 full-length
9	841.4	90.9	1002	4	BM919830 full-length
10	828	88.4	1059	4	BM544445 full-length
11	820.8	88.6	870	5	BM380789 full-length
12	820.2	88.6	1081	4	BM918524 full-length
13	814.8	88.0	934	4	AL576138 full-length
14	813.4	87.8	839	6	CA777979 full-length
15	813.2	87.8	961	1	AL553031 full-length
16	794.6	85.8	996	4	BM559163 full-length
17	793.8	85.7	855	4	CR593062 full-length
18	793.2	85.7	1061	4	BM609372 full-length
19	781.8	84.4	886	1	AL546843 full-length
20	777.8	84.0	1021	4	BM556765 full-length
21	767.8	82.9	856	5	BM373593 full-length
22	758	81.9	830	2	BF568977 full-length
23	758	81.9	836	1	AL525027 full-length
24	753.8	81.4	807	6	CF127550 full-length

25	752.2	81.2	897	4	BG682892
26	750.4	81.0	1128	4	BM541894
27	748.8	80.9	762	7	CR264895
28	738.6	79.8	865	5	EX437235
29	737.2	79.6	994	5	BQ219146
30	736.6	79.5	1129	2	BE621829
31	734.2	79.3	794	7	CR264925
32	733.8	79.2	854	4	B1819212
33	732.8	79.1	939	5	BQ926660
34	729.2	78.7	1083	5	BQ277663
35	727.2	78.5	921	5	BQ222774
36	719.4	77.7	921	5	EX395514
37	719.2	77.7	732	5	BUE25137
38	718.6	77.6	811	1	A1346430
39	718	77.5	886	5	BQ229885
40	717.2	77.5	730	5	BM977684
41	716.4	77.4	807	4	B1255137
42	716.2	77.3	856	5	BQ433990
43	716.2	77.3	886	5	B177698
44	714	77.1	732	7	CN479126
45	713.6	77.1	840	5	BQ940719

ALIGNMENTS

RESULT 1	CR591965	950 bp	mrna	linear	HTC 21-JUL-2004
LOCUS	CR591965	full-length cDNA clone	CSOD1049YN03	of Placenta Cot 25-normalized	
DEFINITION	CR591965	full-length cDNA clone	CSOD1049YN03	of Homo sapiens (human).	
ACCESSION	CR591965	GI:50472772			
VERSION	CR591965.1				
KEYWORDS	HTC; CNSLT_CDNA.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	L.I.W.B., Gruber,C., Jessee,J. and Polayes,D.				
TITLE	Full-length cDNA libraries and normalization				
JOURNAL	Unpublished				
REMARK	Contact: Feng Liang Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com/ invitrogen Corporation 1600 Faraday Avenue 2 (bases 1 to 950)				
REFERENCE	Genoscope.				
AUTHORS	Direct Submission				
TITLE	Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage ;				
JOURNAL	BP 191 91006 EVRY cedex - FRANCE (E-mail: sequef@genoscope.cns.fr				
COMMENT	- Web : www.genoscope.cns.fr) 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by life technologies, a division of invitrogen.				
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Matches	913; Conservative 0; Mismatches 5; Indels 3; Gaps 1;				
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QY	64	CGCGCCGCCGCGGCCCCACGCTTGCCTGAAGGCCGGCAGACAGCAGCGGTCCGGACG	123
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QY	181	GGGCGCGCTGCTGCTGCGCTGCTGGACGAGCAGCAGTAAAGTACTCTCTACGACATGA	240
Db	210	GGGCGCGCTGCTGCGCTGCTGCTGGACGAGCAGCAGTAAAGTACTCTCTACGACATGA	269
QY	241	ACGCGTGTACTCAGCGCTCAGAGAGTGGTGGCCACCTCGCCCAAGACCGAAGTGA	300
Db	270	ACGCGTGTACTCAGCGCTCAGAGAGTGGTGGCCACCTCGCCCAAGACCGAAGTGA	329
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Db	750	GGGGGTGGGATTCACCTGTGTGTTTCAATTTTGAAGAAGACAGACATTTAAAAAATGG	809
QY	781	TCAGGTTGGGCTTCTTCAGATTTCTGAGAAATTTGCTTGTATTGATATTAACAATGAT	840
Db	810	TCAGGTTGGGCTTCTTCAGATTTCTGAGAAATTTGCTTGTATTGATATTAACAATGAT	869
QY	841	CACCGACTGAGAAATATGTTTAACAATAGTCTGAGGGGCGTTTTTTTGTATTAACA	900
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QY	901	AATAATTAGTGGTGA AAA 921	
Db	930	AATAATTAGTGGTGA AAA 950	

RESULT 2	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
CR615862	CR615862	full-length cDNA clone CS0D1026YK10 of Plicenta Cot 25-normalized	CR615862	CR615862	HTC; CNSLT_cDNA.	Homo sapiens (human)	Homo sapiens
		952 bp mRNA linear					
							Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

[illegible]

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QY 661 GAGGCACTGGGCGAGAGAGGGGCGCTCTCTCTGCAACACCTACTAGTCACCAAGACCTTTA 720
DB 692 GAGGCACTGGGCGAGAGAGGGGCGCTCTCTCTGCAACACCTACTAGTCACCAAGACCTTTA 751
QY 721 GGGGGTGGGATTCCTGCTGTGTTTCTATTTTGGAAAAAGACATTTTAAAAATGG 780
DB 752 GGGGGTGGGATTCCTGCTGTGTTTCTATTTTGGAAAAAGACATTTTAAAAATGG 811
QY 781 TCACGTTGGTCTCTCAGATTTCTGAGGAATGCTTTGATTTGATTTACATGAT 840
DB 812 TCACGTTGGTCTCTCAGATTTCTGAGGAATGCTTTGATTTGATTTACATGAT 871
QY 841 CACCGACTGAGAAATTTGTTTACAAATAGTCTGTGGGGCTGTTTTTGTATTAAACA 900
DB 872 CACCGACTGAGAAATTTGTTTACAAATAGTCTGTGGGGCTGTTTTTGTATTAAACA 931
QY 901 AATAATTTAGATGTGAAAAA 921
DB 932 AATAATTTAGATGTGATAA 952

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LOCUS CR599901 970 bp mRNA linear HTC 21-JUL-2004
DEFINITION full-length cDNA clone CSOD1072Y105 of Placenta Cot 25-normalized
ACCESSION CR599901
VERSION CR599901.1 GI:50480708
KEYWORDS HTC; CNSLT_cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
JOURNAL Full-length cDNA libraries and normalization
REMARK Unpublished
Contact: Feng Liang Email: fliang@life.technet.com URL: http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Paraday Avenue 2 (bases 1 to 970)
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail: sequef@genoscope.cns.fr - Web: www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
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Best Local Similarity 99.1%; Pred. No. 2.5e-211;
Matches 913; Conservative 0; Mismatches 5; Indels 3; Gaps 1;

QY 4 GCCCATCTGTTTCAGCCAGTCGCCAAGATCATGAAAGTCCCAAGTGCAGACCGCA 63
DB 50 GCCCATCTGTTTCAGCCAGTCGCCAAGATCATGAAAGTCCCAAGTGCAGACCGCA 109

QY 64 CCGCCGCGCGGGCCCCAGCTGCGGCTGAAAGCCGGCAAGACAGCGGTGCGGGC 123
DB 110 CCGCCGCGCGGGCCCCAGCTGCGGCTGAAAGCCGGCAAGACAGCGGTGCGGGC 169
QY 124 AGGTGTGCGCTGTCTGTCTGAGCAGAGCGTGGCCATCTCGGCTG---CGGGGCGCC 180
DB 170 AGGTGTGCGCTGTCTGTCTGAGCAGAGCGTGGCCATCTCGGCTGCGGGGCGCCG 229
QY 181 GGGGCGCGCTGCGGCTGCGGCTGAGCAGAGCAAGTAAAGTGTGCTTACAGATGA 240
DB 220 GGGGCGCGCTGCGGCTGCGGCTGAGCAGAGCAAGTAAAGTGTGCTTACAGATGA 289
QY 241 ACGGCTGTACTCAGCGCTCAAGAGCTGTGTGCCACCTGCGCCAGAAACGCAAGTGA 300
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DB 350 GCAAGTGAAGATTTCTCAGACGATCATCATCATCAAGGACCTTCAAGTTGAGCTGA 409
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DB 650 AGAACAAGACCGATCGGGCCACTGCGCCCTTAAGTGCATCCAGCTGGGCTGAGCT 709
QY 661 GAGGCACTGGGCGAGAGAGGGGCGCTCTCTGCAACACCTACTAGTCACCAAGACTTTA 720
DB 710 GAGGCACTGGGCGAGAGAGGGGCGCTCTCTGCAACACCTACTAGTCACCAAGACTTTA 769
QY 721 GGGGGTGGGATTCCTGCTGTGTTTCTATTTTGGAAAAAGACATTTTAAAAATGG 780
DB 770 GGGGGTGGGATTCCTGCTGTGTTTCTATTTTGGAAAAAGACATTTTAAAAATGG 829
QY 781 TCACGTTGGTCTCTCAGATTTCTGAGGAATGCTTTGATTTGATTTACATGAT 840
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QY 841 CACCGACTGAGAAATTTGTTTACAAATAGTCTGTGGGGCTGTTTTTGTATTAAACA 900
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QY 901 AATAATTTAGATGTGAAAAA 921
DB 950 AATAATTTAGATGTGATAA 970

RESULT 4
LOCUS CR621997 958 bp mRNA linear HTC 21-JUL-2004
DEFINITION full-length cDNA clone CSOD104YE10 of T cells (Jurkat cell line)
ACCESSION CR621997
VERSION CR621997.1 GI:50502804
KEYWORDS HTC; CNSLT_cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 958)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact: Reng Liang Email: fliang@life.techn.com URL:
http://fulllength.invitrogen.com/Invitrogen Corporation 1600
Paradise Avenue
2 (bases 1 to 958)
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 Evry cedex - FRANCE (E-mail: seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.

REFERENCE
AUTHORS
TITLE
JOURNAL

COMMENT

FEATURES
Source Location/Qualifiers
1..958
/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="CS0D1014E10"
/issue_type="T cells (Jurkat cell line) Cot
10-normalized"
/plasmid="pCMVSPORT_6"

ORIGIN

Query Match 96.7%; Score 895.2; DB 3; Length 958;
Best Local Similarity 99.3%; Pred. No. 7e-211;
Matches 910; Conservative 0; Mismatches 3; Indels 3; Gaps 1;

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43 GCCCATCTGTTTACGACAGTCGCCAAGATCATGAAGTCCGACAGTGCACACCGCA 102
64 CG 123
103 CG 162
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163 AGGTGTGCGCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 222
181 GGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
223 GGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 282
241 ACAGCTGTACTACAGCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 300
283 ACAGCTGTACTACAGCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 342
301 GCAAGGTGAGATTCTCCAGACGTCATCATCATCATCATCATCATCATCATCATCAT 360
343 GCAAGGTGAGATTCTCCAGACGTCATCATCATCATCATCATCATCATCATCATCAT 402
361 ACTCGGAATCCGAATGGAAGACCCCGGGGGGCGAGGGGCTCGGGCTCGGCTCA 420
403 ACTCGGAATCCGAATGGAAGACCCCGGGGGGCGAGGGGCTCGGGCTCGGCTCA 462
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463 GCAAGCTTACAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 522
481 ATCGATTTTGT 540
523 ATCGATTTTGT 582
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DB 643 AGAACAAGACCGATCG 702
QY 661 GAGGCACTGCGGAGAGAGAGCGCGCTCTGTCTGTGACACTTACTAGTACCAGACTTTA 720
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QY 721 GGGGCTGGGATTCACCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 780
DB 763 GGGGCTGGGATTCACCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 822
QY 781 TCACCTTTGCTGCTTCTCAGATTCTGAGAAATTGCTGTGTGTGTGTGTGTGTGTGTGT 840
DB 823 TCACCTTTGCTGCTTCTCAGATTCTGAGAAATTGCTGTGTGTGTGTGTGTGTGTGTGT 882
QY 841 CACGCACTGAGAAATTTGTTTACATATGTTCTGTGTGTGTGTGTGTGTGTGTGTGT 900
DB 883 CACGCACTGAGAAATTTGTTTACATATGTTCTGTGTGTGTGTGTGTGTGTGTGTGT 942
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RESULT 5
AL546878

LOCUS 951 bp mRNA linear EST 25-MAR-2004
DEFINITION Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
ACCESSION clone CS0D1026YK10 5-PRIME, mRNA sequence.
VERSION AL546878
KEYWORDS AL546878.3 GI:45747338
EST.

SOURCE
ORGANISM

Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 951)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:1268711.
COMMENT
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr; Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
10246.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdnafs=CS0D1026YK10&f=10246.f.
Location/Qualifiers
1..951

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/clone="CS0D1026YK10"
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/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

Query Match 95.8%; Score 887.4; DB 1; Length 951;
Best Local Similarity 99.0%; Pred. No. 6e-209;
Matches 912; Conservative 2; Mismatches 3; Indels 4; Gaps 2;

4 GCCCATCTGTTTACGACAGTCGCCAAGATCATGAAGTCCGACAGTGCACACCGCA 63

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Db      32  GCCATTCTGTTTCAGCCAGTCGCCAAGATCATGAAATCCCGCAGTGGCAGACCCGCCA 91
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Db      92  CCGCGCGCGCGGCGCCAGCTCGGGCTAAGAGCCGGCAAGAGAGAGCGGTGGCGGCG 151
Qy     124  AGGTGGTGGCTGTCTGTCTGAGCAGAGCGTGGCCATCTCGGCGT---CCGCGGCGCGCG 180
Db     152  AGGTGGTGGCTGTCTGTCTGAGCAGAGCGTGGCCATCTCGGCGTGGCGGCGCGCG 211
Qy     181  GGGCGCGCGCTGCTGCTGCTGAGCAGCAGCAGAGTAAACGTGCTGCTCTACGACATGA 240
Db     212  GGGCGCGCGCTGCTGCTGCTGAGCAGCAGAGAGTAAACGTGCTGCTCTACGACATGA 271
Qy     241  ACGGCTGTTACTCAGCGCTCAAGAGAGCTGTGCCACCTGCCCAAGAACCGCAAGTGA 300
Db     272  ACGGCTGTTACTCAGCGCTCAAGAGAGCTGTGCCACCTGCCCAAGAACCGCAAGTGA 331
Qy     301  GCAAGGTGAGATTCTCCAGCAGATCATGACATCACTGAGGACCTTGAGTGGAGCTGA 360
Db     332  GCAAGGTGAGATTCTCCAGCAGATCATGACATCACTGAGGACCTTGAGTGGAGCTGA 391
Qy     351  ACTCGGAATCCGAAGTGGGACCCCCGGGGGCGAGGGCTGCGGCTCGCGCTCA 420
Db     392  ACTCGGAATCCGAAGTGGGACCCCCGGGGGCGAGGGCTGCGGCTCGCGCTCA 451
Qy     421  GCAACCTTCAACCGCGAGATCAGCGCCCTGACGCGCGAGCGGCGCATGCGTCTCGGAGC 480
Db     452  GCAACCTTCAACCGCGAGATCAGCGCCCTGACGCGCGAGCGGCGCATGCGTCTCGGAGC 511
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Qy     661  GAGGACAGTGGGAGAGAGGGGCGCTCCTCTGCAACACTACTACTAGTCAACCAAGCTTGA 720
Db     692  GAGGACAGTGGGAGAGAGGGGCGCTCCTCTGCAACACTACTACTAGTCAACCAAGCTTGA 751
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Db     872  CACGACAGAGAAATTTGTTTAAATAGTTCTGTGGGCGTGTGTGTGTTTATTAACA-M 930
Qy     901  AATAATTTAGATGTGAAAAA 921
Db     931  AATAATTTAGATGTGAAAAA 951

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RESULT 6
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LOCUS    CR600217
DEFINITION 939 bp mRNA linear HTC 21-JUL-2004
(human)
ACCESSION CR600217
VERSION   CR600217.1 GI:50481024
KEYWORDS  HTC; cDNA;
SOURCE    Homo sapiens (human)

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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 939)
AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact: Feng Liang Email: fliang@life.rockefeller.edu
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paradise Avenue
2 (bases 1 to 939)
REFERENCE Genoscope.
AUTHORS Direct Submission
TITLE Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
JOURNAL BP 191 91006 Evry cedex - FRANCE (E-mail: seqref@genoscope.cns.fr)
COMMENT - Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and BclI sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
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Matches 881; Conservative 0; Mismatches 3; Indels 3; Gaps 1;
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Db 413 ACTCGGAATCCGAAGTGGGACCCCCGGGGGCGAGGGCTGCGGCTCGCGCTCA 472
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Db	886	GCCCATTTCTGTTTCAGCCAGTCGCCAAGAAATTCAGAAAGTCCGACGTGGCAGACACCGCA	827
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Qy	124	AGGTGATGCGCTGTCTGTCTGTAGACAGACGTCGTGCATCT--CGCGCTGCGCGGGCGCG	180
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[illegible]

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AY	781 TCACTGTTGGTCTCTCAGATTTCTGAGGAAATGCTTGTATTTGATTTTAAATACAT	840

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106 TCACGTTTGTCCTCAGATTTTCAAGGAATTGCCTGGCCGTAAATGCCAATAACTCGTA
840

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CR610338				
Locus				
DEFINITION	CR610338	868 bp	mRNA	linear
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		of Homo sapiens (human).		normalized
Accession				

ACCESSION

KEYWORDS	HTC; CNSLT_CDNA.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Fulvcrvora, Metazoa, Chordata, Mammalia, Primates, Hominidae, Homo

REFERENCE
AUTHORS

1 (bases 1 to 866)

1, W.B., Gruber, C., Jessee, J. and Polaves, D.

Archaea; Bacteria; Eukarya; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Carnivora; Homiidae; Homo.

JOURNAL REMARK	TITLE
Full-length cDNA libraries and normalization unpublished Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue Genoscope - 2 (bases 1 to 868)	REFERENCE AUTHORS JOURNAL
Direct Submision Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : secretef@genoscope.cns.fr - Web : www.genoscope.cns.fr) 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and clone into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. Location/Qualifiers 1..868 /organism="Homo sapiens" /mol_type="mrna" /db_xref="taxon:9606" /clone="CSODID057YJ17" /tissue.type="Placenta Cot 25-normalized" /plasmid="pCMVSPORT_6"	COMMENT
FEATURES source	FEATURES
Query Match 91.1%; Score 844; DB 3; Length 868; Best Local Similarity 99.1%; Pred. No.3,4e-198; Matches 860; Conservative 0; Mismatches 5; Indels 3; Gaps 1	ORIGIN
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Qy	714	GACCTTAGGGGGGGGAGANTCCAGTCGCTGTTCTATTTTGGAAAAGACACATTTTAA	772
Db	661	GACCTTAGGGGGGGGAGANTCCAGTCGCTGTTCTATTTTGGAAAAGACACATTTTAA	720
Qy	774	AAATGTGTCAGTGTGGTCTCTCAGATTTCTGAGGAAATGCTTTGTATTTATATA	833
Db	721	AAATGTGTCAGTGTGGTCTCTCAGATTTCTGAGGAAATGCTTTGTATTTATATA	780
Qy	834	CAATGATCACCGACTGAGATATTTGTTTACAAATGTTCTGTGGGCGTGTTTTGTGA	893
Db	781	CAATGATCACCGACTGAGATATTTGTTTACAAATGTTCTGTGGGCGTGTTTTGTGA	840
Qy	894	TTAAACAATTAATTTAGTGTGTAATAA	921
Db	841	TTAAACAATTAATTTAGTGTGTAATAA	868
RESULT 9			
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LOCUS			
DEFINITION	AGENCOURT_6708266 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5749552		EST 12-MAR-2002
ACCESSION	BM919830		
VERSION	BM919830.1		
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 1002)		
TITLE	NIH-MGC http://mgc.nci.nih.gov/.		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT	Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgabps-remail.nih.gov		
	Tissue Procurement: Life Technologies, Inc.		
	CDNA Library Preparation: Life Technologies, Inc.		
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)		
	DNA Sequencing by: Agencourt Bioscience Corporation		
	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov		
	Plate: LLM12779 row: d column: 09		
FEATURES	High quality sequence stop: 703.		
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	/db_xref="taxon:9606"		
	/clone="IMAGE:5749552"		
	/lab_host="DH10B"		
	/clone_id="NIH_MGC_120"		
	/note="Organ: pooled pancreas and spleen; Vector: pCW-SHORT6; Site 1: NotI; Site 2: EcoRV (destroyed) from 28 yo male. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-2.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 025. Note: this is a NIH_MGC Library."		
ORIGIN			
Query Match	90.9%;	Score 841.4;	DB 4; Length 1002;
Best Local Similarity	97.2%;	Pred. No. 1.5e-197;	
Matches 878;	Conservative 0;	Mismatches 21;	Indels 4; Gaps 2;
Qy	4	GCCCAATCTGTTTCAGCAGTCGCGCAGAAATCATGAAGTCGCGAGTGGGACGACGCCCA	63
Db	31	GCCCAATCTGTTTCAGCAGTCGCGCAGAAATCATGAAGTCGCGAGTGGGACGACGCCCA	90
Qy	64	CCGCGCGCGCGCGCGCGCGCTGCGCTGGAAGCCCGGCAAGACGCGAGCGTGCGGCG	123

[illegible]

AUTHORS NIH-MGC <http://mgc.ncl.nih.gov/>,
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: Invitrogen
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LMNL at:
<http://image.liml.gov>
 Plate: LMNL2723 row: h column: 12
 High quality sequence stop: 705.
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 /db_xref="taxon:9606"
 /clone="IMAGE:5728187"
 /cissue_type="hippocampus"
 /lab_host="DH10B"
 /clone_idb="N1H MGC 124"
 (note="Organ: brain; Vector: pCMV-SPORT6; Site_1: EcoRV
 (destroyed); Site_2: NotI; RNA source male hippocampus,
 age 27. Library is oligo-dT primed and directionally
 cloned (EcoRV site is destroyed upon cloning). Average
 insert size 1.4 kb, insert size range 0.9-4 kb. Library is
 normalized and enriched for full-length clones and was
 constructed by C. Gruber (Invitrogen). Research Genetics
 tracking code 012."

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1081)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: gsapbds-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNLI)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNLI at:
<http://image.llnl.gov>
Plate: LHAM12773 row: 1 column: 18
High quality sequence stop: 626.
Location/Qualifiers
1. 1081
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5747489"
/lab_host="DH10B"
/clone_lib="NIH MGC 120"
/note="Organ: pooled pancreas and spleen; Vector:
pCMV-SPORTc, site_1: NotI, site_2: EcoRV (destroyed), RNA
source anonymous pool of spleen and pancreas from 28 yo
male. Library is oligo-dT primed and directionally cloned
(EcoRV site is destroyed upon cloning). Average insert
size 1.5 kb, insert size range 1-2.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen) Research Genetics
tracking code 025. Note: this is a NIH_MGC Library."

ORIGIN
Query Match 88.6%; Score 820.2; DB 4; Length 1081;
Best Local Similarity 95.7%; Pred. No. 2.8e-192;
Matches 874; Conservative 0; Mismatches 32; Indels 7; Gaps 3;
QY 14 TTTGAGCCAGTGGCCAGATCATGAAAGTGCAGTGGAGCAGCCGCGCCGCCG 73
DB 1 TTTGAGCCAGTGGCCAGATCATGAAAGTGCAGTGGAGCAGCCGCGCCGCCG 60
QY 74 GGGGCCAGCTGCGCGCTGAAGCGCGGGAAGACAGCCGCGTGCAGGCGTGTGCG 133
DB 61 GGGGCCAGCTGCGCGCTGAAGCGCGGGAAGACAGCCGCGTGCAGGCGTGTGCG 120
QY 134 CTGCTGTGTGAGAGAGAGCTGCGCATCTCCGCGTGG--CCGGGGCGCGGGCGCGCT 190
DB 121 CTGCTGTGTGAGAGAGAGCTGCGCATCTCCGCGTGGCGCGGGCGCGCGCGCT 180
QY 191 GCTGTCCTGTGTGAGAGAGAGCTGCGCATCTCCGCGTGGCTTACGACATGAAAGCGCTGTTA 250
DB 181 GCTGTCCTGTGTGAGAGAGAGCTGCGCATCTCCGCGTGGCTTACGACATGAAAGCGCTGTTA 240
QY 251 CTGAGCGCTCAAGAGAGCTGCGCGCAACCTGCGCGGAGCAAGCGCAAGGAGCAAGGTTGA 310
DB 241 CTGAGCGCTCAAGAGAGCTGCGCGCAACCTGCGCGGAGCAAGCGCAAGGTTGA 300
QY 311 GATTCTCAGCAGCTGATCATGACTACATCAGAGGAGCTTCACTGAGTGAAGTGAATCCGGAATC 370
DB 301 GATTCTCAGCAGCTGATCATGACTACATCAGAGGAGCTTCACTGAGTGAAGTGAATCCGGAATC 360
QY 371 CGAAGTTGGAGCCCCCGGGGGCGGAGGCGTCCCGGCTCCGGGCTCCGCTCAGACCCCTCAA 430
DB 361 CGAAGTTGGAGCCCCCGGGGGCGGAGGCGTCCCGGCTCCGGGCTCCGCTCAGACCCCTCAA 420
QY 431 CGGGAGAGTCAAGCGCGCTGAGCGGCGAGGCGGAGTGGCTTCTGCGGAGCGATCCGATCTT 490
DB 421 CGGGAGAGTCAAGCGCGCTGAGCGGCGGAGGCGGAGTGGCTTCTGCGGAGCGATCCGATCTT 480

QY 491 GTGTCGCTGAAGCGCTCTCCCCAGAGGACCGGCGGAGCCCGAGCATCCGAGGGGCGCAGAGG 550
DB 481 GTGTCGCTGAAGCGCTCTCCCCAGAGGACCGGCGGAGCCCGAGCATCCGAGGGGCGCAGAGG 540
QY 551 AATTAGCTGCTCTGTGGGATCTCCCCAAGCGCGCTGCGCGGATCTGAGGAGAAACAAGAC 610
DB 541 AATTAGCTGCTCTGTGGGATCTCCCCAAGCGCGCTGCGCGGATCTGAGGAGAAACAAGAC 600
QY 611 CGATCGCGCGCGCATGTGGCGCCCTTAATCTGATCCAGCCTGGGGGCTGAGAGCTGAGGCACTGG 670
DB 601 CGATCGCGCGCGCATGTGGCGCCCTTAATCTGATCCAGCCTGGGGGCTGAGAGCTGAGGCACTGG 660
QY 671 CGAGAGAGAGGCGCTCCTCTCTGACACCTACTAGTACACAGAGACTTTAGGGGGTGGGA 730
DB 661 CGAGAGAGAGGCGCTCCTCTCTGACACCTACTAGTACACAGAGACTTTAGGGGGTGGGA 720
QY 731 TTCACATCGTGTGTTTCTATTATTTTGGAAAAAGCAGACATTTTAAAAATGTCACGTTTGG 790
DB 721 TCCACTCGNGNGNGTTCTATTATTTTGGAAAAAGCAGACATTTT-AAAAATGTCACGTTTGG 779
QY 791 TGCCTTCAGATTTCTGAGGAAATGCTTGTATGTATATTTCAATGATCACCGACTGA 850
DB 780 TGCCTTCAGATTTCTGAGGAAATGCTTGTATGTATATTTCAATGATCACCGACTGA 839
QY 851 GAATATTGTTTACATATGTTTC--TGTGGGCGCTGTTTTTTGTTATTATTAACAATATATT 907
DB 840 AAATATTGTTTAAATGTTTCCCTGTCGTGGGGCGCTGTTTTTTGGAATTAACCAATATATT 899
QY 908 TAGATGTGTAATA 920
DB 900 TAGATGTGGAATA 912

RESULT 13
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LOCUS
DEFINITION AL576138 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CSOD1072Y105 3-PRIME, mRNA sequence.
ACCESSION AL576138
VERSION AL576138.3 GI:46249018
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 934)
AUTHORS Li, W.-B., Gruber, C., Jesssee, J., and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 16, 2001 this sequence version replaced gi:31314429.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
10246.f
For more information about this cluster, see
<http://www.genoscope.cns.fr/cdna?b=CSOD1072AR03NP1&c=10246.f>.
Location/Qualifiers
1. 934
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/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V

ORIGIN sites of the PCWVSPORT 6 vector. Library was normalized."

Query Match 88.0%; Score 814.8; DB 1; Length 934;
 Best Local Similarity 95.8%; Pred. No. 5.9e-191;
 Matches 849; Conservative 4; Mismatches 29; Indels 4; Gaps 2;

QY 4 GCCCATCTGTTTCCAGCCAGTCCGCAAGATCATGAAATCGCCAGTGGACACCGGCA 63
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 DB 826 MCSGCGCGCGGAGCCCGCCAGCTCGCGCTGAAGCCGCGCAAGACAGCGTGGCGGCG 767
 QY 124 AGGTGTGCGCTGTCTGTCTGACAGAGCGTGGCATCT--CGGCTGCGCGCGCGCG 180
 DB 766 AGGTGTGCGCTGTCTGTCTGACAGAGCGTGGCATCTCTTCCGCGCTGCGCGCGCG 707
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 DB 706 GGGCGCGCTGCTGCTGCTGCTGACAGACAGAGTAAAGTGTGCTTACGACATGA 647
 QY 241 ACGGCTGTACTCAGCGCTCAAGAGAGTGTGCCACCTGCGCCGCAAGACGCAAGTGA 300
 DB 646 ACGGCTGTACTCAGCGCTCAAGAGAGTGTGCCACCTGCGCCGCAAGACGCAAGTGA 587
 QY 301 GCAAGGTGAGATTTCTCCAGCAGCTGATGACTACATCAGGAGAC--CTTACATTTGAGCTG 359
 DB 586 GCAAGGTGAGATTTCTCCAGCAGCTGATGACTACATCAGTGTGAGTGGAGCTG 527
 QY 360 AACTGGATCCGAAAGTTGGAGACCCCGGCGGCGCAAGGCTGCGGCTCGGCTCGCTC 419
 DB 526 TACTGGAATCCGAAGTTGGAACCCCGGCGGCGCAAGGCTGCGGCTCGGCTCGCTC 467
 QY 420 AGCACCTTCAACGCGAGATCAAGCGCTGACGCGCGCAAGCGCATGCTTCTGCGAGC 479
 DB 466 AGCACCTTCAACGCGAGATCAAGCGCTGACGCGCGCAAGCGCATGCTTCTGCGAGC 407
 QY 480 GATCGCATCTTGTGTGCTGAAGCGGCTTCCCAAGGAGCCGCGGAGACCCAGCCATCCAG 539
 DB 406 GATCGCATCTTGTGTGCTGAAGCGGCTTCCCAAGGAGCCGCGGAGACCCAGCCATCCAG 347
 QY 540 GGGGGAAGAGAAATTAAGTGTGCTGAGGCTTCCCCCAAGCGGCTTCCCGCGGATCTGAGG 599
 DB 346 GGGGGAAGAGAAATTAAGTGTGCTGAGGCTTCCCCCAAGCGGCTTCCCGCGGATCTGAGG 287
 QY 600 GAGAACAGACCGATCGGCGGCGCATGCGCCCTTAAGTGCATCGAGCGTGGGGCTGAGGCG 659
 DB 286 GAGAACAGACCGATCGGCGGCGCATGCGCCCTTAAGTGCATCGAGCGTGGGGCTGAGGCG 227
 QY 660 TGAGGCACTGGGAGAGAGAGGCGCTCTCTGTGACACCTAAGTGCATCGAGACTTT 719
 DB 226 TGAGGCACTGGGAGAGAGAGGCGCTCTCTGTGACACCTAAGTGCATCGAGACTTT 167
 QY 720 AGGGGTTGGGATTTCACTGTGTGTTTCTAATTTTGAAGACAGACATTTAAATAATG 779
 DB 166 AGGGGTTGGGATTTCACTGTGTGTTTCTAATTTTGAAGACAGACATTTAAATAATG 107
 QY 780 GTACAGTTGGTCTTCTCAGATTTCTGAGAAATTTGTTTATTTGATATATTACATGA 839
 DB 106 GTACAGTTGGTCTTCTCAGATTTCTGAGAAATTTGTTTATTTGATATATTACATGA 47
 QY 840 TCACCGACTGAGATATTTGTTTAACTAATATGTTCTGTGGGGCTGTTT 885
 DB 46 TCACCGACTGAGATATTTGTTTAACTAATATGTTCTGTGGGGCTGTTT 1

RESULT 14
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 LOCUS l1p1b11.x1 HR85 islet Homo sapiens cDNA clone IMAGE:6217316 3'
 DEFINITION similar to SW:ID1_HUMAN P41134 DNA-BINDING PROTEIN INHIBITOR ID-1

ACCESSION CA777979
 VERSION CA777979.1 GI:26015854
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
 AUTHORS
 1 (bases 1 to 839)
 Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemshka,I., Scaer,M., Brestelli,J., Gradwohl,G., Clifton,S., Hillier,L., Maira,M., Pape,D., Wylie,T., Martin,J., Bliscain,A., Schmit,A., Theising,B., Ritter,E., Ronco,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T., Jackson,Y. and Bowers,Y.
 Endocrine Pancreas Consortium
 Unpublished (2000)
 CONTACT: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
 Harvard University, Howard Hughes Medical Institute
 Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138
 Tel: 617-495-1812
 Fax: 617-495-8557
 Email: dmelton@biohp.harvard.edu

LIBRARY was constructed by Dr. Hiroshi Inoue DNA sequencing by: Washington University Genome Sequencing Center for information on obtaining a clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
 Seq primer: -40UP from Gibco
 High quality sequence atp: 447.

FEATURES
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6217316"
 /tissue_type="Purified pancreatic islet"
 /lab_host="DH10B"
 /clone_id="HR85 islet"
 /note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1: NotI; Site_2: XhoI; cDNA made by oligo-dT priming. Size-selected on agarose gel. Average insert size ~1kb. 5' XhoI site was destroyed after directional cloning. Amplified once. Contact information: Hiroshi Inoue, MD, Metabolism Div. (Alan Permutt Lab), Washington University School of Medicine, Box 8127, 660 South Euclid Ave., St. Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel: 314-362-1916, Fax: 314-747-2692."

ORIGIN

Query Match 87.8%; Score 813.4; DB 6; Length 839;
 Best Local Similarity 96.9%; Pred. No. 1.3e-190;
 Matches 830; Conservative 0; Mismatches 6; Indels 3; Gaps 1;

QY 84 TGGCGCTGAAGGCGCGCAAGACAGCGAGCGTGGCGGCGAGGTGCTGCTGTCT 143
 DB 839 TGGCGCTGAAGGCGCGCAAGACAGCGAGCGTGGCGGCGAGGTGCTGCTGTCT 780
 QY 144 GAGCGAGCGGCGCATCTGCGGCTG---CGGGGCGCGCGGGCGCGCTGCGGCTG 200
 DB 779 GAGCGAGCGGCGCATCTGCGGCTGCGGCGCGGGGCGCGGGCGCGCTGCGGCTG 720
 QY 201 CTGACGAGCAGCAGGTAAAGTGTGCTTACGACATGAACGCTGTACTCAGCGCTC 260
 DB 719 CTGACGAGCAGCAGGTAAAGTGTGCTTACGACATGAACGCTGTACTCAGCGCTC 660
 QY 261 AAGAGCTGTGCTCCACCTTCCCAAGAACCGCAAGGTGAGCAAGGTGAATTTCTCAG 320
 DB 659 AAGAGCTGTGCTCCACCTTCCCAAGAACCGCAAGGTGAGCAAGGTGAATTTCTCAG 600
 QY 321 CACGTCATGACATCAGAGGACCTTCAATTGAGCTGGAAGCTGCACTCGAATTCGAAGTTGG 380

Db 599 CACGTCATGCACTACATCAGGAGCCTTCAGTTGAGCTGAACCTCGAATTCGAAGTGG 540
 QY 381 ACCCCCGGGGGCCGAGGGCTGCGGCTCGGGCTCGGCTCAGCACTCTTAACGGGAGATC 440
 Db 539 ACCCCCGGGGGCCGAGGGCTGCGGCTCGGGCTCGGCTCAGCACTCTTAACGGGAGATC 480
 QY 441 AGCGCTCAGCGGCGGAGCGGATGCGTTCCTGCGGAGCAATCGCATCTTGTGTGCTGA 500
 Db 479 AGCGCTCAGCGGCGGAGCGGATGCGTTCCTGCGGAGCAATCGCATCTTGTGTGCTGA 420
 QY 501 AGCGCTCCTCCCGAGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 560
 Db 419 AGCGCTCCTCCCGAGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 360
 QY 551 TCTGTGGGTCTCCCGAGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 620
 Db 359 TCTGTGGGTCTCCCGAGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 300
 QY 621 CCACCTGCGCCTTAACTGATCAGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 680
 Db 299 CCACCTGCGCCTTAACTGATCAGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 240
 QY 681 GCGCTCTCTCTGCAACCTACTAGTCAACAGACCTTAAAGGGGTGGGATTCACCTCTGT 740
 Db 239 GCGCTCTCTCTGCAACCTACTAGTCAACAGACCTTAAAGGGGTGGGATTCACCTCTGT 180
 QY 741 GTGTTTCTATTTTGAAGAGCAGCATTTTAAAGATGTGCTGCTGCTGCTGCTGCTGCTGCT 800
 Db 179 GTGTTTCTATTTTGAAGAGCAGCATTTTAAAGATGTGCTGCTGCTGCTGCTGCTGCTGCT 120
 QY 801 ATTTGTGAGAAATGCTTTGATGTATATATATACATGATCAACGAGTGAATATGTT 860
 Db 119 ATTTGTGAGAAATGCTTTGATGTATATATATACATGATCAACGAGTGAATATGTT 60
 QY 861 TTACATATGTTCTGTGGGCTGTGTTTGTATTTAAACAATATATTTAGTGTGA 919
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RESULT 15
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 LOCUS AL553031 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
 DEFINITION clone CS0D1072Y105 5-PRIME, mRNA sequence.
 ACCESSION AL553031 GI:45857801
 VERSION AL553031.3
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 1 (bases 1 to 961)
 Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 On Feb 15, 2001 this sequence version replaced gi:31274845.
 COMMENT
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dt) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen. This sequence belongs to sequence cluster
 10246.f

For more information about this cluster, see
 http://www.genoscope.cns.fr/cdnas=CS0D1072AB03P1ec-10246.f.
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 Source
 Location/Qualifiers
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 /mol_type="mRNA"
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/clone="CS0D1072Y105"
 /tissue_type="PLACENTA COT 25-NORMALIZED"
 /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo(dt)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 87.8%; Score 813.2; DB 1; Length 961;
 Best Local Similarity 95.7%; Pred. No. 1.5e-190;
 Matches 880; Conservative 10; Mismatches 19; Indels 11; Gaps 5;

QY 4 GCCATTCTGTTTACGACGATCGCCAGATCATGAAGTCCGACGAGGACCGGCA 63
 Db 50 GCCATTCTGTTTACGACGATCGCCAGATCATGAAGTCCGACGAGGACCGGCA 109
 QY 64 CCGCGCGCGGGGCCCGAGCTGCGCGCTGAAGGCGGCAAGACAGCGGCTGCGGGCG 123
 Db 110 CCGCGCGCGGGGCCCGAGCTGCGCGCTGAAGGCGGCAAGACAGCGGCTGCGGGCG 169
 QY 124 AGTGTGCGCTGTCTGTCTGAGCAGAGCGTGGCCATCTGCGCTG--CCGGGGCGCG 180
 Db 170 AGTGTGCGCTGTCTGTCTGAGCAGAGCGTGGCCATCTGCGCTGCGCGGGCGCG 229
 QY 181 GGGCGCGCTGCGCTGCGCTGAGCAGAGCGTGAAGCGTGAAGCGTCTGTAAGCAATGA 240
 Db 230 GGGCGCGCTGCGCTGCGCTGAGCAGAGCGTGAAGCGTGAAGCGTCTGTAAGCAATGA 289
 QY 241 ACGGCTGTACTCAAGCTCCTAAGAGCTGTGCTCCACCTGCGCCCAAGCGCAAGGTGA 300
 Db 290 ACGGCTGTACTCAAGCTCCTAAGAGCTGTGCTCCACCTGCGCCCAAGCGCAAGGTGA 349
 QY 301 GCAAGGTGAGATTTCTCAGACGTCATCGACTACAGAGGACCTTCAAGTGAAGCTGA 360
 Db 350 GCAAGGTGAGATTTCTCAGACGTCATCGACTACAGAGGACCTTCAAGTGAAGCTGA 409
 QY 361 ACTGGAATCCGAAGTTGGGACCCCGGGGGCGAGGGGCTGCGGGCTGCGGGCTGCGCTCA 420
 Db 410 ACTGGAATCCGAAGTTGGGACCCCGGGGGCGAGGGGCTGCGGGCTGCGGGCTGCGCTCA 469
 QY 421 GCAACCTCAACGCGAGATCAGCGCCTGACGCGCGGAGGCGGAGCTTCTGCGGAG 480
 Db 470 GCAACCTCAACGCGAGATCAGCGCCTGACGCGCGGAGGCGGAGCTTCTGCGGAG 529
 QY 481 ATGCGATCTTGTGTGCTGAGAGCGCTCTCCCAAGGACCGGCGGACCCCAAGCTTCAAG 540
 Db 530 ATGCGATCTTGTGTGCTGAGAGCGCTCTCCCAAGGACCGGCGGACCCCAAGCTTCAAG 589
 QY 541 GGGCAAGAGAAATTAAGTGTCTGTGGGTCTCCCAAGGAGGCTGCGCGGATGAGGG 600
 Db 590 GGGCAAGAGAAATTAAGTGTCTGTGGGTCTCCCAAGGAGGCTGCGCGGATGAGGG 649
 QY 601 AGAACAAGACCGATCGCGCGGACATGCGCCTTAATGCAATCCAGCTGCGGGCTGAGGCT 660
 Db 650 AGAACAAGACCGATCGCGCGGACATGCGCCTTAATGCAATCCAGCTGCGGGCTGAGGCT 709
 QY 661 GAGGCACTGCGGAGAGAGGGGCTCTCTGTGCAACCTAATGTAACAGAGACTTTA 720
 Db 710 GAGGCACTGCGGAGAGAGGGGCTCTCTGTGCAACCTAATGTAACAGAGACTTTA 769
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 Db 770 GGGGGTGGGAAATTCACGTCGTGTCTTATTTTGAAGGACACATTTTAAAAATGG 828
 QY 781 TCAGTTTGTGCTTCTCAGATTTCTGAGAAATGCTGTGTAATGTAATTAATGAT 840
 Db 829 TCAGTTTGTGCTTCTCAGATTTCTGAGAAATGCTGTGTAATGTAATTAATGAT 887
 QY 841 CACGCACTGAGATATTTGTTTACATATGTTCTGTGGGCTGTTTTTTTGTATTAACA 900
 Db 888 CACGCACTGAGATATTTGTTTACATATGTTCTGTGGGCTGTTTTTTTGTATTAACA 941

Oy 901 AATAATTAGATGTGAAA 920
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Db 942 AATAATTADRTGKGAAAA 961

Search completed: December 18, 2004, 20:21:47
Job time : 3377.83 secs

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GenCore version 5.1.6
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OW nucleic - nucleic search, using sw model

Run on: December 18, 2004, 13:51:20 ; Search time 5373.66 Seconds
(without alignments)
10586.727 Million cell updates/sec

Title: US-09-996-529A-5

Perfect score: 1203
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:*
1: gb_ba:*
2: gb_hvg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
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9: gb_pr:*
10: gb_ro:*
11: gb_sgs:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1178.4	98.0	1203	9 HSHLHR21	X69111 H.sapiens H
2	885.4	72.6	976	6 BC003107	BC003107 Homo sapi
3	856.2	71.2	982	6 A17546	A17546 H.sapiens m
4	856.2	71.2	982	6 I59693	I59693 Sequence 1
5	856.2	71.2	982	6 I72140	I72140 Sequence 1
6	856.2	71.2	982	6 AX63639	AX63639 Sequence
7	856.2	71.2	982	6 HSHRIRA	X66924 H.sapiens h
8	854	71.0	957	11 BVI78372	BVI78372 sqm10012
9	730	60.7	1903	6 AB056417	AB056417 Macaca fa
10	663.8	55.2	2481	6 AX578014	AX578014 Sequence
11	652.8	54.3	129722	9 H515005	X73428 H.sapiens I
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13	462	38.4	969	10 MUSHLH462	M60523 Mouse helix
14	460.4	38.3	983	10 BC064658	BC064658 Rattus no
15	377.2	31.4	497	4 CFA271644	AJ271644 Canis fam
16	360	29.9	360	6 A17548	A17548 H.sapiens m
17	360	29.9	360	6 CQ727798	CQ727798 Sequence
18	360	29.9	360	6 I59694	I59694 Sequence 3
19	360	29.9	360	6 I72141	I72141 Sequence 3

20	358.4	29.8	360	6 AX481474	AX481474 Sequence
21	358	29.8	360	9 BR006791	BR006791 Homo sapi
22	358	29.8	360	12 BR007901	BR007901 Synthetic
23	349.6	29.1	227074	2 AC060772	AC060772 Mus muscu
24	349.6	28.7	568	10 AL935264	AL935264 Mous DNA
25	345.8	25.7	495	6 CQ056982	CQ056982 Sequence
26	309	25.7	495	6 CQ076246	CQ076246 Sequence
27	309	25.7	495	6 CQ107235	CQ107235 Sequence
28	309	25.7	495	6 CQ145905	CQ145905 Sequence
29	309	25.7	495	6 CQ181357	CQ181357 Sequence
30	309	25.7	495	6 CQ205696	CQ205696 Sequence
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32	309	25.7	495	6 CQ267236	CQ267236 Sequence
33	309	25.7	495	6 CQ304261	CQ304261 Sequence
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41	222	18.5	427	11 BV104787	BV104787 MARC 5747
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ALIGNMENTS

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LOCUS
DEFINITION H.sapiens HLH 1R21 mRNA for helix-loop-helix protein.
ACCESSION X69111 S55813
VERSION X69111.1 GI:32294
KEYWORDS
SOURCE
ORGANISM
Homo sapiens
Homo sapiens (human)
helix-loop-helix protein.

REFERENCE
AUTHORS
TITLE
1 (bases 1 to 1203)
Deed,R.W., Bianchi,S.M., Atherton,G.T., Johnston,D.,
Santibanez-Koref,M., Murphy,J.D., and Norton,J.D.
An immediate early human gene encodes an id-like helix-loop-helix
protein and is regulated by protein kinase C activation in divers
cell types

JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
Oncogene 8 (3), 599-607 (1993)

JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
2 (bases 1 to 1203)
Deed,R.W., Hirose,T., Mitchell,E.L., Santibanez-Koref,M.F. and
Norton,J.D.

JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
Structural organisation and chromosomal mapping of the human Id-3
gene
Gene 151 (1-2), 309-314 (1994)

JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
7828896
3 (bases 1 to 1203)
Deed,R.

JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
Direct Submission
Submitted (04-NOV-1992) R. Deed, Paterson Inst for Cancer Research,
Dept of Gene Regulation, Christie Hospital NHS Trust, Wilmslow
Road, Manchester, M20 9BX, UK

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Location/Qualifiers
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Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Sanchez,A., Whiting,M., Kettelman,M., Madan,A., Rodriguez,S., Bouffard,G.G., Blakeley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butcherfield,Y.S., Krzywinski,M.I., Skalska,U., Smillius,D.E., Scherch,A., Schein,J.E., Jones,S.J. and Marra,M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences Proc. Natl. Acad. Sci. U.S.A. 99 (26) , 16899-16903 (2002)

2 (bases 1 to 976)

JOURNAL
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL

Strausberg,R.
Direct Submission
Submitted (13-Feb-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgapdb-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTF
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butcherfield, Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao, Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin, Teika Olson, Diana Palmqvist, Anca Petrescu, Anna Liisa Prahbu, Parvaneh Saedi, Jr Santos, Angelique Scherch, Ursula Skalska, Duane Smalius, Jeff Stott, Miranda Tsai, George Yang, Jacque Schein, Asim Siddiqui, Rob Holt, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL ac: <http://image.lnl.gov>
Series: IRAL Plate: 8 Row: a Column: 24.
Location/Qualifiers

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CDS
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Query Match 73.6%; Score 885.4; DB 9; Length 976;
Best Local Similarity 99.6%; Pred. No. 2.6e-195;
Matches 919; Conservative 0; Mismatches 1; Indels 3; Gaps 3;

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QY 462 CGGCACTGAGAGAGCGCGTGAAGCTTGTGAGCAGATGAACCATCTTACCTCCGCTGC 521
Db 181 CGGCACTGAGAGAGCGCGTGAAGCTTGTGAGCAGATGAACCATCTTACCTCCGCTGC 240
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RESULT 3
LOCUS A17546 982 bp RNA linear PAT 17-MAR-1994
DEFINITION H.sapiens mRNA HEIR-1 (neuroblastoma-associated regulator).
ACCESSION A17546
VERSION A17546.1 GI:490012
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 982)
REFERENCE
AUTHORS
TITLE
JOURNAL
Patent: WO 9313205-A 1 08-JUL-1993;
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ORIGIN

Query Match 71.2%; Score 856.2; DB 6; Length 982;
Best Local Similarity 97.7%; Pred. No. 1.7e-188;
Matches 900; Conservative 0; Mismatches 18; Indels 3; Gaps 3;
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40 GATCTGACACACGAGGAACTCAAGCACTTCTTTCTTTCTTTCTTTCTTTGGG 99
344 GCACCTTGACACTCATCTCCCAAGCATGAAAGCGCTGAGCCGCGCGCTGTACAG 403
100 GCACCTTGACACTCATCTCCCAAGCATGAAAGCGCTGAGCCGCGCGCTGTACAG 159
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Best Local Similarity 97.7%; Pred. No. 1.7e-188;
Matches 900; Conservative 0; Mismatches 18; Indels 3; Gaps 3;
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ORIGIN
Query Match 71.2%; Score 856.2; DB 6; Length 982;
Best Local Similarity 97.7%; Pred. No. 1.7e-188;
Matches 900; Conservative 0; Mismatches 18; Indels 3; Gaps 3;
ORIGIN
284 GAGCGTGGCGCGCTTCAGGTCACTGTAGCGGACTTCTTTGGTTTCTTTCTTTGGG 343
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DEFINITION Sequence 1 from patent US 5683878.
ACCESSION 172140
VERSION 172140.1 GI:3008279
KEYWORDS
SOURCE .
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 982)
AUTHORS Ellmeier,W. and Welch,A.
TITLE Neuroblastoma-associated regulator gene
JOURNAL Patent: US 5683878-A 1 04-NOV-1997;
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ORIGIN
Query Match 71.2%; Score 856.2; DB 6; Length 982;
Best Local Similarity 97.7%; Freq. No. 1.7e-188;
Matches 900; Conservative 0; Mismatches 18; Indels 3; Gaps 3;

QY 284 GAGCGTGGCGGCTGTGACGCTGACGCTGACGAGCTTCTTTGGTTTCTCTTTGGG 343
DB 40 GATCTGCAACGAGGAACTTCAAGCACTTCTTTGGTTTCTCTTTGGG 99
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QY 1123 GTATATAGTTTGTGACCTTTTATACAGGAAAGTGTCTGTATACATGCGATGAT 1182
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QY 1183 ATTAACCTTTTATTAAGTT 1203
DB 938 ATTAACCTTTTATTAAGTT 958

RESULT 6
LOCUS AX663639 982 bp DNA linear PAT 22-MAR-2003
DEFINITION Sequence 14 from Patent WO02097127.
ACCESSION AX663639
VERSION AX663639.1 GI:29163847
KEYWORDS
SOURCE .
ORGANISM Homo sapiens (human)
REFERENCE 1
AUTHORS Oellers,N., Gehrmann,M., Kallabis,H., Hall,R., Schulze,T. and Kroegel,C.
TITLE Genes and proteins for prevention, prediction, diagnosis, prognosis and treatment of chronic lung disease

JOURNAL Patent: WO 02097127-A 14 05-DEC-2002;
Bayer Aktiengesellschaft (DE)
Location/Qualifiers
1.982
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Query Match 71.2%; Score 856.2; DB 6; Length 982;
Best Local Similarity 97.7%; Pred. No. 1.7e-188;
Matches 900; Conservative 0; Mismatches 18; Indels 3; Gaps 3;

284 GAGCGTGGCGCGCTGGCAAGTCACTGTAGCGGACCTCTTTGGTTTCTTCTTTGGG 343
40 GATCCTGCACACCGGAACTCA CAGACACCTTCTTTGGTTTCTTCTTTGGG 99
344 GCACCTGCGACCTACTCTCCAGATATAGGCGCTGAGCCGGTGCCTGCTACGAG 403
100 GCACCTGCGACCTACTCTCCAGATATAGGCGCTGAGCCGGTGCCTGCTACGAG 159
404 GCGGTGTCTGCTGTCTGCAAGCAAGTCTGCGCCATGCGCCCGGGCCGAGGAGGCGCCG 463
160 GCGGTGTCTGCTGTCTGCAAGCAAGTCTGCGCCATGCGCCCGGGCCGAGGAGGCGCCG 219
464 GCGGTGTCTGCTGTCTGCAAGCAAGTCTGCGCCATGCGCCCGGGCCGAGGAGGCGCCG 523
220 GCGGTGTCTGCTGTCTGCAAGCAAGTCTGCGCCATGCGCCCGGGCCGAGGAGGCGCCG 279
524 GAACTGTGATCCCGGAGTCCCGGAGGCACTCACTTATAGCAAGTATCTTAAGAGCGC 583
280 GAACTGTGATCCCGGAGTCCCGGAGGCACTCACTTATAGCAAGTATCTTAAGAGCGC 339
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704 GACAAAGAGAGCTTTTGCACACTGCTGCGCCGTCTCTGCAACCTTCCAGAAAGCGAGTGC 763
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764 TGGCGCCGCTTCTGCTGCGGAGCCCGGGAACCTTCTTCCGGAAGCGGAGCGGAGGGA 823
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QY 1183 ATTAACCTTTATATAAGTT 1203
DB 938 ATTAACCTTTATATAAGTT 958

RESULT 7
LOCUS HSHRIRA 982 bp mRNA linear PRI 18-NOV-1993
DEFINITION H.sapiens helr-1 mRNA for helix-loop-helix protein.
ACCESSION X66924.S40308
VERSION X66924.1 GI:395337
KEYWORDS helix-loop-helix protein.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 982)
Elmeier,W., Aguzzi,A., Kleiner,E., Kurzbauner,R. and Weith,A.
Mutually exclusive expression of a helix-loop-helix gene and N-myc
in human neuroblastomas and in normal development
EMBO J. 11 (7), 2563-2571 (1992)
JOURNAL MEDLINE PUBMED
92331608
1628620
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CDS

Query Match 71.2%; Score 856.2; DB 9; Length 982;
Best Local Similarity 97.7%; Pred. No. 1.7e-188;
Matches 900; Conservative 0; Mismatches 18; Indels 3; Gaps 3;

284 GAGCGTGGCGCGCTGGCAAGTCACTGTAGCGGACCTCTTTGGTTTCTTCTTTGGG 343
40 GATCCTGCACACCGGAACTCA CAGACACCTTCTTTGGTTTCTTCTTTGGG 99
344 GCACCTGCGACCTACTCTCCAGATATAGGCGCTGAGCCGGTGCCTGCTACGAG 403
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404 GCGGTGTCTGCTGTCTGCAAGCAAGTCTGCGCCATGCGCCCGGGCCGAGGAGGCGCCG 463
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584 GTGATGCACTAATTTCTGCACTGCAAGTATCTTGGCCGAGCCAGCCCTTGAACCCCT 643
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644 GATGCCCCCACTTCCCATCCAGACGCGGAGCTTGTCCGGAACCTTGTCACTTCCAC 703

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TITLE Genes involved in osteogenesis, and methods of use
JOURNAL Percent: WO 02081745-A 136 17-OCT-2002;
Aventis Pharma S.A. (FR)
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Best Local Similarity 99.7%; Pred. No. 1.1e-143;
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DB 372 GATCTGGGGTGTCTGCCAGAAAAGCAATTCTGGAAGTTATGTTTGAATGATCTT 431
QY 61 AAATCTTGCTGGCGAGAGAGCCCGCTCTCCCGGATCAGCGGCTTCTCAATCTTGA 120
DB 432 AAATCTTGCTGGCGAGAGAGCCCGCTCTCCCGGATCAGCGGCTTCTCAATCTTGA 491
QY 121 ATCCGCGGCTCCGCGGTCTTTCGCGCTCAGACCGCGAGAGAGCTGTTTCAATTGA 180
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DEFINITION H.sapiens Id3 gene for HLH type transcription factor.
ACCESSION X73428.1 GI:313212
VERSION X73428.1
KEYWORDS early response gene; transcriptional factor.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1
AUTHORS Deed,R.W., Hirose,T., Mitchell,E.L., Santibanez-Koref,M.F. and Norton,J.D.
TITLE Structural organisation and chromosomal mapping of the human Id-3 gene
JOURNAL Gene 151 (1-2), 309-314 (1994)
MEDLINE 95129881
PUBMED 7828896
REFERENCE 2 (bases 1 to 2481)
AUTHORS Deed,R.
TITLE Direct Submission
JOURNAL Submitted (18-JUN-1993) R. Deed, Paterson Institute for Cancer Research, Dept of Gene Regulation, Christie Hospital NHS Trust, Wilmslow Road, Manchester, M20 9BX, UK
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Query Match 55.2%; Score 663.8; DB 9; Length 2481;
Best Local Similarity 99.7%; Pred. No. 1.1e-143;
Matches 665; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GATCTGGGGTGTCTGCCAGAAAAGCAATTCTGGAAGTTATGTTTGAATGATCTT 60
DB 372 GATCTGGGGTGTCTGCCAGAAAAGCAATTCTGGAAGTTATGTTTGAATGATCTT 431
QY 61 AAATCTTGCTGGCGAGAGAGCCCGCTCTCCCGGATCAGCGGCTTCTCAATCTTGA 120
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repeat_region	11493. .11748
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repeat_region	11784. .12089
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repeat_region	12257. .12541
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Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Buterfield, Y.S., Krzywinski, M.I., Skalska, U., Smal, D.E., Schermer, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

2 (bases 1 to 983)
12477932

JOURNAL
PUBMED
REFERENCES
AUTHORS
TITLE
JOURNAL

Strausberg, R.
Direct Submission
Submitted (22-DEC-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
Contact: MGC help desk
Email: cgabds-r@mail.nih.gov
Tissue Procurement: Dr. Maarten Bosland, NYU
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc.mgc@nih.gov

Akher, N., Ayale, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakeley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Latic, P., Legaspi, R., Maduro, Q.L., Masello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantrop, S., Thomas, P.J., Touchman, J.W., Tsougen, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>
Series: IRAX Plate: 137 Row: P Column: 16
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6961073.
Location/Qualifiers

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Best Local Similarity 77.5%; Pred. No. 2.3e-96;
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147 CGCTGAGCTGTGAGCAGATGAACTCATCTGCTCCCGCTGCGGGAACGTGATCCG 206
537 GAGTCCGAGAGGCGCTGAGCTGAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGG 596
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1156 GTGACTTTCTGTACATGCGATGTATATTAACCTTTTATTAAGTT 1203
864 GTGACTTTCTGTACATGCGATGTATATTAACCTTTTATTAAGTT 911

RESULT 15
CFA271644 497 bp mRNA linear MM 01-OCT-2002
LOCUS Cantis familiaris mRNA for ID3 protein (ID3 gene).
DEFINITION AJ271644
ACCESSION AJ271644
VERSION AJ271644.1 GI:6782310
KEYWORDS Id3 gene, Id3 protein.
SOURCES Cantis familiaris (dog)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1

AUTHORS
TITLE

Deleu, S., Savonnet, V., Behrendts, J., Dumont, J.E. and Maenhaut, C. Study of gene expression in thyrotropin-stimulated thyroid cells by cDNA expression array: I03 transcription modulating factor as an early response protein and tumor marker in thyroid carcinomas *Exp. Cell Res.* 279 (1), 62-70 (2002)

PUBMED
REFERENCE

12213214
2 (bases 1 to 497)

TITLE
JOURNAL

Direct Submission
Submitted (25-JAN-2000) Delau S., Iribm, Institute of
interdisciplinary research, 808 Route de Lemnik, Bruxelles, 1070,
BELGIUM

FEATURES

source	location/Qualifiers
1. .497	1. .497
	/organism="Canis familiaris"
	/mol_type="mRNA"
	/db_xref="taxon:9615"
	/tissue_type="Thyroid"
	/clone_id="Lambda zapII"
gene	1. .497
	/gene="ID3"
CDS	76. .435

ORIGIN

Query Match	31.4%;	Score 377.2;	DB 4;	Length 497;
Best Local Similarity	89.3%;	Pred. No. 5e-77;		
Matches 418; Conservative	0;	Mismatches 48;	Indels 2;	Gaps 1

OY 324 TGGTTTCTTCTCTTTGGGGCACCTTGGACCTACTCCACGACATGAAAGCGCTGAACC 383
 Db 32 TGGCTCTCTCTCTCTCTTGGGACCTCCGGGCTCACTCTGCATATTTGAAGCGCTGAAGCC 91
 OY 384 CGGTGCGGCGTGTCTAGAGAGCGGATGTGCTGCTGTGCAGAAAGCAGTCTGGCCATTCGCC 443
 Db 92 CGGTGCGGCGTGTCTAGAGAGCGGATGTGCTGCTGTGCAGAGCAGCTGGCCATTCGCC 151
 OY 444 GGGGCGCAGAGAGAGGCGCCGCGACCTGAGAGAGCGCTGAGCTTGTCTGACACATGAAAC 503
 Db 152 GCGGAGCGCGGAGAGGCGCCCGGCGCGGAGAGAGCGCTGTGAGCTGTTTGGACACATGAAAC 211
 OY 504 ACTGTACTCCCGCGCTGCGGGAACCTGTATCCCGAGTCCCGAGAGGCACTCAAGTTTACC 563
 Db 212 ACTGTACTCGCGCTTGTGCGGAACTGTATCCCGAGTCCCGAGAGCACTCAAGTTTACC 271
 OY 564 AGGTGGAATCTTACAGCGCGCTATCGACTACATTCTTGACCTGAGGTAGTCTTGCGCG 623
 Db 272 AGGTGGAATCTTACAGCGCGCTATCGACTACATTCTTGACCTGAGGTAGTCTTGCGCG 331
 OY 624 AGCAGCGCCCTTGAACCCCTTGATGGGCGCCCACTTCCCATCCAAACAGCGGAGTCTGC 683
 Db 332 AGCGCGGCCCTTGACCCCGCCGAGCGCGGCATCTTCCCATCCAAACAGCGGAGTCTGC 391
 OY 684 CGGAATCTGTCACTTCCAAAGCAAGAAAGAGCTTTTGCACTGACCTGAGCGCTGTCTTA 743
 Db 392 CGGAATCTGTGATCTTCCAAAGCAAGAAAGAGCTTGTGCACTGACCTGAGCG--AGCCTTG 449
 OY 744 CACCTCCAGAACGACAGGTGCTGAGCGCCGCTTCTGTCTGGAGACCCCGG 791
 Db 450 CGGCTCCAGAACCGAGGTCTGAGCGCCGCTTCTGTCTGGAGACCCCGG 497

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 18, 2004, 13:49:15 ; Search time 660.548 Seconds
(without alignments)
9560.323 Million cell updates/sec

Title: US-09-996-529A-5

Perfect score: 1203
Sequence: 1 gatcgggggtctgcgcagga.....ttaacttttataaagct 1203

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4134866 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: geneseqn2003s:*
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8: geneseqn2005s:*
9: geneseqn2006s:*
10: geneseqn2007s:*
11: geneseqn2008s:*
12: geneseqn2009s:*

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1178.4	98.0	1203	6	ABQ88115 Human ost
2	1178.4	98.0	1203	6	ADH28990 Human chr
3	1164.2	96.8	2066	9	ACH04136 Human CDN
4	1164.2	96.8	2066	10	ADU56457 Human CDN
5	1162.8	96.7	1300	3	AA121652 Human bre
6	870.2	72.3	3372	8	ACC46300 Human dit
7	856.2	71.2	982	2	AAQ44245 HEIR-1 ge
8	856.2	71.2	982	6	ABQ88114 Human ost
9	856.2	71.2	982	10	ACC46763 Human COP
10	856.2	71.2	982	12	AD124462 Human mod
11	856.2	71.2	982	12	AD182868 Human PRO
12	663.8	55.2	2481	6	ABQ88116 Human ost
13	663.8	55.2	2481	8	ABZ34778 Coding se
14	662.8	54.3	129722	6	ABQ88117 Human ost
15	652.8	54.3	129722	12	AD018027 Human sof
16	522.8	43.5	3372	8	ACC46300 Human dit
17	498.4	41.3	510	10	ADK11708 Breast ca
18	496.4	41.3	522	10	ADK11707 Breast ca
19	437.8	36.4	653	12	ABE77049 Human CDN
20	437.8	36.4	2066	9	ACH04136 Human CDN
21	437.8	36.4	2066	10	ADU56457 Human CDN

22	434.2	36.1	1447	12	ADQ22623 Human sof
23	425	35.3	465	9	ACH44238 Human foe
24	423.6	35.1	429	9	ACH21548 Human adu
25	358.4	29.8	360	6	ABV78204 Human ID3
26	358.4	29.8	360	6	ABZ35780 Human ID3
27	358.4	29.8	360	6	ABX10023 Human ID3
28	358.4	29.8	360	6	ABL91745 Human pol
29	358.4	29.8	360	12	AD000370 Novel hum
30	358.4	29.8	360	12	ADN98801 Novel hum
31	354	29.4	531	12	ACH76426 Human gen
32	345.8	28.7	568	10	AB141893 Toxicity
33	335.4	27.9	517	6	ABQ39801 Oligonuc
34	335.4	27.9	517	6	ABQ39800 Oligonuc
35	309	25.7	495	4	AA122113 Probe #12
36	309	25.7	495	4	ABA67192 Human foe
37	309	25.7	495	4	AA147408 Probe #16
38	309	25.7	495	4	ABA49278 Human bre
39	309	25.7	495	4	ABA34287 Probe #12
40	309	25.7	495	4	AAK41370 Human bon
41	309	25.7	495	4	AAK15636 Human bra
42	309	25.7	495	4	ABE40961 Human liv
43	309	25.7	495	5	AA107811 Probe #78
44	309	25.7	495	6	AB15375 Human gen
45	306.4	25.5	446	2	AAQ44247 HEIR-1 ge

ALIGNMENTS

RESULT 1	ABQ88115	standard; CDNA; 1203 BP.
XX	ABQ88115;	
XX	18-SEP-2002 (first entry)	
XX	Human osteoblast differentiation related cDNA SEQ ID NO 22.	
XX	Human; osteoblast; stem cell differentiation; bone tissue deposition;	
XX	osteoporosis; osteopathic; ss.	
XX	Homo sapiens.	
XX	WO200250301-A2.	
XX	27-JUN-2002.	
XX	18-DEC-2001; 2001WO-US048276.	
XX	18-DEC-2000; 2000US-0255882P.	
XX	24-APR-2001; 2001US-0285691P.	
XX	(GENE-) GENE LOGIC INC.	
XX	(PROC) PROCTER & GAMBLE CO.	
XX	Ji D, Axelrod DW, Cook US, Jaiswal N, Einstein R, Houghton A;	
XX	Mertz L;	
XX	WPI; 2002-557663/59.	
XX	Use of genes and their expression profiles associated with osteoblast	
XX	differentiation for screening modulators bone formation, for diagnosing	
XX	or treating e.g. osteoporosis, or as markers for the differentiation	
XX	process.	
XX	Claim 1; SEQ ID NO 22; 78pp + Sequence Listing; English.	
XX	The invention relates to genes and their expression profiles are used	
XX	for: (a) screening modulators of precursor stem cell differentiation into	
XX	osteoblasts, or bone tissue deposition; (b) diagnosing abnormal	
XX	deposition of bone tissue, abnormal rate of osteoblast formation or	
XX	osteoporosis; or (c) treating or monitoring treatment of the conditions	

CC cited in (b), or monitoring the progression of bone tissue deposition.
 CC Specific conditions include postmenopausal osteoporosis, glucocorticoid
 CC osteoporosis or male osteoporosis, osteopenia, osteodystrophy, drug-
 CC induced abnormalities in bone formation or bone loss, conditions that
 CC involve altered bone metabolism (e.g., idiopathic juvenile osteoporosis),
 CC skeletal disease linked to breast cancer, mastocytosis, Fanconi syndrome,
 CC or fibrous dysplasia. The present sequence is that of an osteoblast
 CC differentiation associated CDNA marker of the invention. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pat_sequences

Sequence 1203 BP; 233 A; 353 C; 350 G; 267 T; 0 U; 0 Other;

Query Match 98.0%; Score 1178.4; DB 6; Length 1203;
 Best Local Similarity 99.8%; Pred. No. 1.4e-310;

Matches 1201; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

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QY 1 GATCTGGGGTCTCTCCAGGAAAAAGCAATTTCTGAAAGTTAATGTTTGAATGATTTCTT 60
Db 1 GATCTGGGGTCTCTCCAGGAAAAAGCAATTTCTGAAAGTTAATGTTTGAATGATTTCTT 60
QY 61 AATCTTGTCTGGGAGAGGCGGCTCTCCCGGTATACGCGCTTCTCATTTTGA 120
Db 61 AATCTTGTCTGGGAGAGGCGGCTCTCCCGGTATACGCGCTTCTCATTTTGA 120
QY 121 ATCCGCGCTCCGCGGCTTCTCGGCTCAGACCAAGCCGAGAGAGCCGTTTGCATTTAA 180
Db 121 ATCCGCGCTCCGCGGCTTCTCGGCTCAGACCAAGCCGAGAGAGCCGTTTGCATTTAA 180
QY 181 GCGGCGCTGTAAAGCCCAAGGCGCGCGGCGGCGGCGCGAGCGGCGCATTTTGAATTA 240
Db 181 GCGGCGCTGTAAAGCCCAAGGCGCGCGGCGGCGGCGCGAGCGGCGCATTTTGAATTA 240
QY 241 GAGGCGCTGCTTCCAGGAGAGCTCTAATAGTGAACGCGCGGCGAGCGGCGCGGCTTC 300
Db 241 GAGGCGCTGCTTCCAGGAGAGCTCTAATAGTGAACGCGCGGCGAGCGGCGCGGCTTC 300
QY 301 AGGTCACTGTAGGAGGACTTTTGTGTTTCTTTTCTTTTGGGAGCACTCTGAGTCACT 360
Db 301 AGGTCACTGTAGGAGGACTTTTGTGTTTCTTTTCTTTTGGGAGCACTCTGAGTCACT 360
QY 361 CCCAGCATGAAGAGCGCTAGCGCGGTGCGGCGCTACAGAGGCGGTGCTGCTGTC 420
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QY 421 GGAAGCACTGTGCGCATGCGCGGCGCGAGGAAAGGCGCGGAGCTGAGAGCGCGCT 480
Db 421 GGAAGCACTGTGCGCATGCGCGGCGCGAGGAAAGGCGCGGAGCTGAGAGCGCGCT 480
QY 481 GAGCTTGTGAGAGCATGAACCACTGCTACCTCCGCTTGGGAGAACTGTACCGGAGT 540
Db 481 GAGCTTGTGAGAGCATGAACCACTGCTACCTCCGCTTGGGAGAACTGTACCGGAGT 540
QY 541 CCCGAGAGGCACTGAGCTTAAAGCAGGTGAAATCTTACAGGCGCTCATGCACTATTCT 600
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QY 601 GAGCTGAGAGGTGCTGCGCGAGGCGAGCGCGCTTGAACCTCTGATGAGCTTCC 660
Db 601 GAGCTGAGAGGTGCTGCGCGAGGCGAGCGCGCTTGAACCTCTGATGAGCTTCC 660
QY 661 CATCCAGACAGCCAGCTGCTCCGAGAACTTGTCAATCTCCAGAGCAAAAGAGCTTTTG 720
Db 661 CATCCAGACAGCCAGCTGCTCCGAGAACTTGTCAATCTCCAGAGCAAAAGAGCTTTTG 720
QY 721 CCAGTGAATCGGCGGTGCTTGAACCTTCCAGAAAGAGGTGCTGCGCGCTTCTGCT 780
Db 721 CCAGTGAATCGGCGGTGCTTGAACCTTCCAGAAAGAGGTGCTGCGCGCTTCTGCT 780
QY 781 GGGAGCCCGGAGAACTTCTCTGCGGAGAGCGGAGCGGAGGAGTGGCCCACTTCCGCC 840
Db 781 GGGAGCCCGGAGAACTTCTCTGCGGAGAGCGGAGCGGAGGAGTGGCCCACTTCCGCC 840

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QY 841 CTGGCCACTGTACTTACCAAAATCCCTTCTGAGACTTAAACTGTGCTCAGAGCGAA 900
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QY 901 GGAAGTGAATCTTGTAGCTGAGAGGAGGAGGAGTGTGCTGCGGAGCGGAGCGT 960
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QY 961 GAGCTGCTCCACCCGAGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1020
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QY 1021 GAGAGTGTGCTCTTCAAACTATGCAAGGCGGCGGAGGAGGAGGAGGAGGAGG 1080
Db 1021 GAGAGTGTGCTCTTCAAACTATGCAAGGCGGCGGAGGAGGAGGAGGAGGAGG 1080
QY 1081 GAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1139
Db 1081 GAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1139
QY 1140 CTTTCTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1199
Db 1141 CTTTCTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1199
QY 1200 AGTT 1203
Db 1200 AGTT 1203

RESULT 2
ADH28990
ID ADH28990 standard; DNA; 1203 BP.
XX
AC ADH28990;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human chronic myelogenous leukaemia (CML) gene marker #258.
XX
KW de; chronic phase chronic myelogenous leukaemia; CP-CML;
KW blast crisis CML; BC-CML; human; chronic myelogenous leukaemia;
KW gene marker.
XX
OS Homo sapiens.
XX
PN US2003104426-A1.
XX
PD 05-JUN-2003.
XX
PF 14-JUN-2002; 2002US-00171581.
XX
PR 18-JUN-2001; 2001US-0298914P.
XX
PA (LINS/) LINSLEY P S.
PA (MAOM/) MAO M.
PA (DAIR/) DAI H.
PA (HEYY/) HE Y.
PA (RADJ/) RADICH J P.
PI Linsley PS, Mao M, Dai H, He Y, Radich JP;
XX
DR WPI; 2003-787046/74.
XX
PT Classifying cell sample as chronic phase chronic myelogenous leukemia or
PT blast crisis chronic myelogenous leukemia by detecting difference in
PT expression of genes corresponding to the markers such as X15415, U89436.
XX
PS Disclosure; SEQ ID NO 258; 31pp; English.
XX
CC The invention relates to a method of classifying a cell sample as chronic
CC phase chronic myelogenous leukaemia (CP-CML) or blast crisis CML (BC-
CC CML). The method is useful for classifying a sample as CP-CML or BC-CML.

```


CC The present sequence represents a human chronic myelogenous leukaemia
CC (CML) gene marker used to distinguish blast crisis CML from chronic phase
CC CML.
XX

Sequence 1203 BP, 233 A; 353 C; 350 G; 267 T; 0 U; 0 Other;

Query Match 98.0%; Score 1178.4; DB 10; Length 1203;
Best Local Similarity 99.8%; Pred. No. 1.4e-310;
Matches 1201; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

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QY 1 GATCTGGGGTGTCTCCAGGAAAAAGCAATTCTGAAAGTTAATGTTTGTAGTGAATCTT 60
DB 1 GATCTGGGGTGTCTCCAGGAAAAAGCAATTCTGAAAGTTAATGTTTGTAGTGAATTTT 60
QY 61 AAATCTTGTCTGGCGAGAGGCGCGCTCTCCCGGTATCAGCGCTTCTCATTTCTTTGA 120
DB 61 AAATCTTGTCTGGCGAGAGGCGCGCTCTCCCGGTATCAGCGCTTCTCATTTCTTTGA 120
QY 121 ATCCGCGGCTCCGCGGTCTTCCGCGTCAGACACGCGAGGAAAGCTGTTTGCATTTAA 180
DB 121 ATCCGCGGCTCCGCGGTCTTCCGCGTCAGACACGCGAGGAAAGCTGTTTGCATTTAA 180
QY 181 GCGGGCTGTGAACGCCACAGGCGCGCGGGGCGGGGCGGAGGCGGCGCATTTTGAATAA 240
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QY 301 AGGTACTGTAGCGGAGCTCTTTGGTTTCTTTCTTTGGGGGACCTCTGACTCACT 360
DB 301 AGGTACTGTAGCGGAGCTCTTTGGTTTCTTTCTTTGGGGGACCTCTGACTCACT 360
QY 361 CCCGACATGAAGGCGCTGAGGCCGCGTGCAGCTGTACGAGGCGGTGTGCTGCTGTC 420
DB 361 CCCGACATGAAGGCGCTGAGGCCGCGTGCAGCTGTACGAGGCGGTGTGCTGCTGTC 420
QY 421 GGAAGCGAGTCTGGCCTATGCCCCGGGCGCGAGGAAAGGCGCGGCACTGAGAGCCGT 480
DB 421 GGAAGCGAGTCTGGCCTATGCCCCGGGCGCGAGGAAAGGCGCGGCACTGAGAGCCGT 480
QY 481 GAGCTTGTGCGAGCATGTAACCACTGCTACCTCCGCGCGGGAAGCTGTATCCGGAAGT 540
DB 481 GAGCTTGTGCGAGCATGTAACCACTGCTACCTCCGCGCGGGAAGCTGTATCCGGAAGT 540
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DB 541 CCGGAGGCGACTGAGCTTGGCAGGTGGAATCTCTACGCGCGTATGACTGACTATCT 600
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DB 781 GGGAGCGCGGAACTTCTTCTGCGGAGCGCGAGCGGCAAGGATGGGCCCAACTTTCGC 840
QY 841 CTGGCCACTTGACTTACCAAAATCCCTTCTGGAAGCTAAACCTGGTGTCTGAGGCGAA 900
DB 841 CTGGCCACTTGACTTACCAAAATCCCTTCTGGAAGCTAAACCTGGTGTCTGAGGCGAA 900
QY 901 GGAAGTGAATTTGAGCTTGAAGAGCGAGAGCTAGCTTGGCCACAGCTGGGCGAGCT 960
DB 901 GGAAGTGAATTTGAGCTTGAAGAGCGAGAGCTAGCTTGGCCACAGCTGGGCGAGCT 960
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QY 961 CACCTGTCTCCACCCCAAGTTCTTAAGTCTTTTCAGAGCGTGAAGTGTGGA 1020
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DB 1021 GAGAGTGTCTCTCAAACTATGCAAGGCGCGGCGAGCTGTCTTGTGTCCTT 1080
QY 1081 GAGAGAGTGTCTGTGCGCTGATTTATGAACCTATATATG-GTATATAGTTTGTAC 1139
DB 1081 GAGAGAGTGTCTGTGCGCTGATTTATGAACCTATATATGAGTATATAGTTTGTAC 1140
QY 1140 CTTTTTACAGGAAGTGAAGCTTCTGTATGCAATGCGATATATTAACCTTTTATATA 1199
DB 1141 CTTTTTACA-GGAAGTGAAGCTTCTGTATGCAATGCGATATATTAACCTTTTATATA 1199
QY 1200 AGTT 1203
DB 1200 AGTT 1203
```

RESULT 3
ACH04136
ID ACH04136 standard; cDNA; 2066 BP.

ACH04136;
26-SEP-2003 (first entry)

Human cDNA differentially expressed in lung cancer #341.

Gene therapy; emphysema; se; gene; chronic obstructive pulmonary disease;
respiratory disorder; lung cancer; asthma; human.

Homo sapiens.

US2003065157-A1.

03-APR-2003.

04-APR-2002; 2002US-00116802.

04-APR-2001; 2001US-0281593P.

(LASE/) LASEK A W.

Lasek AW;

WPI; 2003-540803/51.

New combination comprising cDNAs that are differentially expressed in
respiratory disorders, useful for diagnosing or treating respiratory
disorders e.g., lung cancer, chronic obstructive pulmonary disease,
emphysema or asthma.

Claim 1; Page: 39pp; English.

The invention relates to a combination comprising cDNAs or their
complements that are differentially expressed in respiratory disorder.
The combination is useful for preparing a composition for diagnosing or
treating respiratory disorders e.g., lung cancer, chronic obstructive
pulmonary disease, emphysema or asthma. The present sequence represents
human cDNA differentially expressed during lung cancer

Sequence 2066 BP; 446 A; 564 C; 594 G; 455 T; 0 U; 7 Other;

Query Match 96.8%; Score 1164.2; DB 9; Length 2066;
Best Local Similarity 99.5%; Pred. No. 1.3e-306;
Matches 1199; Conservative 0; Mismatches 3; Indels 3; Gaps 3;

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QY 1 GATCTGGGGTGTCTCCAGGAAAAAGCAATTCTGAAAGTTAATGTTTGTAGTGAATCTT 60
|||
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QY	1	GATCTGGGAGTGTCTGCCAGAGAAAAAGCAAAATTTCTGGAAGTTAATGTTTTGAGTATTTCTT	60
Db	176	GATCTGGGAGTGTCTGCCAGAGAAAAAGCAAAATTTCTGGAAGTTAATGTTTTGAGTATTTCTT	235
QY	61	AAATTCCTTGTCTGGGCGAGAGAGGCCGCGCTCTCCCGGATATCAGCGCTTCTCATTTCTTGA	120
Db	236	AAATTCCTTGTCTGGGCGAGAGAGGCCGCGCTCTCTCCCGGATATCAGCGCTTCTCATTTCTTGA	295
QY	121	ATCCGCGGCTCCGCGGTCTTTCGGCGTCAAGCCAGCCGAGAGAGCTGTGTTGCAATTTAA	180
Db	296	ATCCGCGGCTCCGCGGTCTTTCGGCGTCAAGCCAGCCGAGAGAGCTGTGTTGCAATTTAA	355
QY	181	GCGGGCTGTGAACGCGCCAGGGCGCGGCGGGGCGGGGCGGAGCGGGGCCATTGTAATTA	240
Db	356	GCGGGCTGTGAACGCGCCAGGGCGCGGCGGGGCGGGGCGGAGCGGGGCCATTGTAATTA	415
QY	241	GAGGCGTGCCTTCCAGGAGGCTCTAATAAGTACCGCGCGGCGAGCGTGC	300
Db	416	GAGGCGTGCCTTCCAGGAGGCTCTAATAAGTACCGCGCGGCGAGCGTGC	475
QY	301	AGGTACACTGTAGC - GGAATTTCTTTTGGTTTTCTTCTTTTGGGGCACTTGTGAATTCAC	358
Db	476	AGGTACACTGTAGCGGGAATTTCTTTTGGTTTTCTTCTTTTGGGGCACTTGTGAATTCAC	535
QY	360	TCCCCAGCATAAAGCGCTGTAGACC CGGCGCGCGCTGCTACGAGCGGTGTGCTGCTGT	419
Db	536	TCCCCAGCATAAAGCGCGCTGTAGACC CGGCGCGCGCTGCTACGAGCGGTGTGCTGCTGT	595
QY	420	CGGAAACGAGTCTGTGGCCATCGCCCGCGGGCGAGGGAAGGCGCCGCGACGTGAGAGCGCG	479
Db	596	CGGAAACGAGTCTGTGGCCATCGCCCGCGGGCGAGGGAAGGCGCCGCGACGTGAGAGCGCG	655
QY	480	TGAGCTTGTGTGAAGCAATGAACAATGTACTCCGCTGTGCGGGAACTGGTATACCGGAG	539
Db	656	TGAGCTTGTGTGAAGCAATGAACAATGTACTCCGCTGTGCGGGAACTGGTATACCGGAG	715
QY	540	TCCGAGAGGGAACCTCAGCTTATAGCAGAGTGAATACTTAACAGCGGCTCATCATTACATTC	599
Db	716	TCCGAGAGGGAACCTCAGCTTATAGCAGAGTGAATACTTAACAGCGGCTCATCATTACATTC	775
QY	600	TCGACCTGTGAAGTATCTGTGGCCGAGGACGAGCCCTTGAACCCCTGATATGACCCCACTTC	659
Db	776	TCGACCTGTGAAGTATCTGTGGCCGAGGACGAGCCCTTGAACCCCTGATATGACCCCACTTC	835
QY	660	CCATCCAGACAGCGAGCTCGCTCCGGAATCTGTATCTCCACGACAAAGAGACTTTT	719
Db	836	CCATCCAGACAGCGAGCTCGCTCCGGAATCTGTATCTCCACGACAAAGAGACTTTT	895
QY	720	GCCACTGACTCGGCGGTGTCTGTGACACCTTCAGAAACGAGGTGTCTGGGCGCCGTTGCC	779
Db	896	GCCACTGACTCGGCGGTGTCTGTGACACCTTCAGAAACGAGGTGTCTGGGCGCCGTTGCC	955
QY	780	TGGGACCCCGGGGAACCTCTCCGCGGGAAGCGGACCGCAGGAGTATGGGCCCCCACTTCCG	839
Db	956	TGGGACCCCGGGGAACCTCTCTCGCGGGAAGCGGACCGCAGGAGTATGGGCCCCCACTTCCG	1015
QY	840	CTGTGCCCACTTGAATTCACAAATCCCTTCTCTGAGACTAAACCTGTGTCTCAGAGAGGA	899
Db	1016	CTGTGCCCACTTGAATTCACAAATCCCTTCTCTGAGACTAAACCTGTGTCTCAGAGAGGA	1075
QY	900	AGGACTGTGAACCTTGTAGCTGTGAAGAGCCAGAGCTAAGTCTTGGCCACCAAGCTGGGCGAG	959
Db	1076	AGGACTGTGAACCTTGTAGCTGTGAAGAGCCAGAGCTAAGTCTTGGCCACCAAGCTGGGCGAG	1135
QY	960	TCAACCTGTCTCCACCCCAACCCCAAGTTCTTAAGTCTTTTCAGAGCTGTGAGGTTGTGA	1019
Db	1136	TCAACCTGTCTCCACCCCAACCCCAAGTTCTTAAGTCTTTTCAGAGCTGTGAGGTTGTGA	1195
QY	1020	AGGATGTGCTGTCTTCCAAACTATGCAAGGCGCGGCGAGACTGTGTCTTCTGTCTTCT	1079
Db	1196	AGGATGTGCTGTCTTCCAAACTATGCAAGGCGCGGCGAGACTGTGTCTTCTGTGTCTTCT	1255

Qy	1080	TGAGAAAGGTTCTGTTGCCCTGATTTATGAACTCTATTAAG-GTATATAGTTTGTGA	1138
Db	1256	TTGGAGAAAGGTTCTGTTGCCCTGATTTATGAACTCTATTAAGGTATATAGTTTGTGA	1315
Qy	1139	CCCTTTTTCACGGGAAAGGTGACTTCTGTATCAATGACGATATATTTAACTTTTATPAA	1198
Db	1316	CCCTTTTTCACGGAAGGTGACTTCTGTATCAATGACGATATATTTAACTTTTATPAA	1374
Qy	1199	AAAGTT 1203	
Db	1375	AAAGTT 1379	
RESULT 5			
AAAF21652			
ID	AAF21652	standard; DNA; 1300 BP.	
AC	AAF21652;		
DT	27-MAR-2001	(first entry)	
DE	Human breast and ovarian cancer associated antigen gene SEQ ID 39.		
XX	Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive;		
KM	nootropic; neuroprotective; antiviral; antiallergic; hepatotropic;		
KM	antidiabetic; antiinflammatory; antitumor; vulnery; anticonvulsant;		
KM	antibacterial; antifungal; antiparasitic; cardiant; immune disorder;		
KM	Addison's disease; allergy; autoimmune haemolytic anaemia;		
KM	autoimmune thyroiditis; diabetes mellitus; Crohn's disease;		
KM	multiple sclerosis; rheumatoid arthritis; ulcerative colitis;		
KM	cardiovascular disorder; wound healing; neurological disease; ds.		
XX			
OS	Homo sapiens.		
PN	WO200055173-A1.		
PD	21-SEP-2000.		
PF	08-MAR-2000; 2000WO-US005881.		
PR	12-MAR-1999; 99US-0124270P.		
PA	(HUMA-) HUMAN GENOME SCI INC.		
PI	Rosen CA, Ruben SM;		
DR	WPI; 2000-611515/58.		
DR	P-PSDB; AAB58749.		
XX			
PT	New human breast and ovarian cancer associated gene sequences and the		
PT	polypeptides encoded by these genes, useful in the prevention, treatment		
PT	and diagnosis of cancer, immune disorders, cardiovascular disorders and		
XX	neurological diseaseaa.		
XX			
PS	Claim 1; Page 509-510; 1299pp; English.		
CC	Sequences AAF21614 - AAF22031 represent DNA sequences encoding human		
CC	proteins AAB58711 - AAB59128. The DNA and protein sequences are		
CC	associated with breast and ovarian cancer. Included in the invention are		
CC	sequences AAF22032 - AAF22040 and AAB59129 which are used in the		
CC	isolation and characterisation of the DNA and protein sequences of the		
CC	invention. The breast and ovarian cancer associated DNA, protein, agonist		
CC	or antagonist sequences exhibit cytostatic; immunosuppressive; nootropic;		
CC	neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic;		
CC	antiinflammatory; antitumor; vulnery; anticonvulsant; antibacterial;		
CC	antifungal; antiparasitic and cardiant activity. The polynucleotide and		
CC	protein sequences are used in the diagnosis of cancer, particularly		
CC	breast and ovarian cancer. The nucleic acid sequences, proteins, agonists		
CC	and agonists may also be used in the diagnosis, prevention and treatment		
CC	of immune disorders e.g. Addison's disease, allergies, autoimmune		
CC	haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's		
CC	disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis;		
CC	cardiovascular disorders such as myocardial ischaemias; wound healing;		

CC neurological diseases such as cerebral anoxia and epilepsy; and
 CC infectious diseases
 XX
 SQ Sequence 1300 BP; 272 A; 368 C; 372 G; 280 T; 0 U; 8 other;

Query Match 96.7%; Score 1162.8; DB 3; Length 1300;
 Best Local Similarity 99.1%; Pred. No. 2.6e-306;
 Matches 1194; Conservative 5; Mismatches 3; Indels 3; Gaps 3;

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QY 1 GATCTGGGGGCTCTGCAAGAAAAAGCAAAATCTGAAAGTAAATGTTTGAATGATCTT 60
DB 31 GATCTGGGGGCTCTGCAAGAAAAAGCAAAATCTGAAAGTAAATGTTTGAATGATCTT 90
QY 61 AAATCTTGTGCGGAGAGGCGCGCTCTCCCGATCAGCGCTTCCATTTTGA 120
DB 91 AAATCTTGTGCGGAGAGGCGCGCTCTCCCGATCAGCGCTTCCATTTTGA 150
QY 121 ATCCGGGCTCCGGGCTTCTTGGCTGAACCAAGCCGAGAGAAAGCTTTGCAATTTAA 180
DB 151 ATCCGGGCTCCGGGCTTCTTGGCTGAACCAAGCCGAGAGAAAGCTTTGCAATTTAA 210
QY 181 GCGGGCTGTGAAGCGCCAGAGGCGCGGGGGCGGGCGCGGCGCATTTTGAATPAA 240
DB 211 GCGGGCTGTGAAGCGCCAGAGGCGCGGGGGCGGGCGCGGCGCATTTTGAATPAA 270
QY 241 GAGGCGTGTCTCCAGGCAAGCTCTATAGTGAACCGCGCGGAGAGCTGCGCGCTTGC 300
DB 271 GAGGCGTGTCTCCAGGCAAGCTCTATAGTGAACCGCGCGGAGAGCTGCGCGCTTGC 330
QY 301 AGGTCACTGTAGC-GGACTTTTGGTTTCTTTTCTTTTGGGCGCACTTGTGACTCAC 359
DB 331 AGGTCACTGTAGGCGGACTTTTGGTTTCTTTTCTTTTGGGCGCACTTGTGACTCAC 390
QY 360 TCCCAACATGAAGGCGCTGAGCGCGGTGCGGCTGTAACAAGGCGGTGCTGCTCT 419
DB 391 TCCCAACATGAAGGCGCTGAGCGCGGTGCGGCTGTAACAAGGCGGTGCTGCTCT 450
QY 420 CGGAACGCACTTGGGCTATGCGCGCGCGGAGGAGGCGCGGAGCTGAGAGCGCG 479
DB 451 CGGAACGCACTTGGGCTATGCGCGCGCGGAGGAGGCGCGGAGCTGAGAGCGCG 510
QY 480 TGAAGCTTGTGAGCAATGAACCACTGCTACCCCGCTGCGGGAACCTGTGACCGGAG 539
DB 511 TGAAGCTTGTGAGCAATGAACCACTGCTACCCCGCTGCGGGAACCTGTGACCGGAG 570
QY 540 TCCCGAGAGGCACTGCTTAAAGCAAGTGAATCTTCAAGCGCTCATCGACTATTC 599
DB 571 TCCCGAGAGGCACTGCTTAAAGCAAGTGAATCTTCAAGCGCTCATCGACTATTC 630
QY 600 TGAAGCTTGTGAGCAATGAACCACTGCTACCCCGCTGCGGGAACCTGTGACCGGAG 659
DB 631 TGAAGCTTGTGAGCAATGAACCACTGCTACCCCGCTGCGGGAACCTGTGACCGGAG 690
QY 660 CCATCCAGACAGCCGAGCTGCTCCGGAATTTGATCTTCAACGACAAAGAGCTTTT 719
DB 691 CCATCCAGACAGCCGAGCTGCTCCGGAATTTGATCTTCAACGACAAAGAGCTTTT 750
QY 720 GGCACGAGCTGGGCGCTGCTGCAACCTTCCAGAAAGCAAGTGTGCGCGCTTCTGCC 779
DB 751 GGCACGAGCTGGGCGCTGCTGCAACCTTCCAGAAAGCAAGTGTGCGCGCTTCTGCC 810
QY 780 TGGGAGCCCGGAGAACCTTCTGCGGAGAGCGGAGCGGAGAGTGGGCGCCCACTTCC 839
DB 811 TGGGAGCCCGGAGAACCTTCTGCGGAGAGCGGAGCGGAGAGTGGGCGCCCACTTCC 870
QY 840 CCGTCCCACTTGAATTCACAAATCTTCTTGTGAAGTAAACCTGTTGCTCAGAGCGA 899
DB 871 CCGTCCCACTTGAATTCACAAATCTTCTTGTGAAGTAAACCTGTTGCTCAGAGCGA 930
QY 900 AGGACTGTGAACCTTGTAGCTGAAGAGCAGAGTAACTGTGCGACACAGCTGGGCGAG 959
DB 931 AGGACTGTGAACCTTGTAGCTGAAGAGCAGAGTAACTGTGCGACACAGCTGGGCGAG 990

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QY 960 TCACCTGTCTCCACCCACCCCAAGTCTTAAAGTCTTTTCAAGAGCTGAGAGTGGGA 1019
DB 991 TCACCTGTCTCCACCCACCCCAAGTCTTAAAGTCTTTTCAAGAGCTGAGAGTGGGA 1050
QY 1020 AGGAGTGTCTGTCTTCCAACTATGCGAGGCGCGGAGAGTGTCTTCTGCTCTCT 1079
DB 1051 AGGAGTGTCTGTCTTCCAACTATGCGAGGCGCGGAGAGTGTCTTCTGCTCTCT 1110
QY 1080 TGGAGAAAGTTCGTGGTCCCTGATTTATGAACTTATATAG-GTATATAGTTTTTGA 1138
DB 1111 TGGAGAAAGTTCGTGGTCCCTGATTTATGAACTTATATAGTATATAGTTTTTGA 1170
QY 1139 CTTTTTTACAGGAGGAGTGACTTTCTGTAAACATGATGATATTAATTTTATTA 1198
DB 1171 CTTTTTTACA-GGAGAGTGACTTTCTGTAAACATGATGATATTAATTTTATTA 1229
QY 1199 AAGTT 1203
DB 1230 AAGTT 1234

```

RESULT 6
 ACC46300/c
 ID ACC46300 standard; cDNA, 3372 BP.

ACC46300;

02-JUN-2003 (first entry)

Human dthp transcription factor-encoding cDNA.

Human; dthp; diagnostic and therapeutic polypeptide; diagnosis;
 cancer; cell proliferative disorder; autoimmune disorder;
 inflammatory disorder; infection; hormonal disorder; metabolic disorder;
 neurological disorder; gastrointestinal disorder; transport disorder;
 connective tissue disorder; drug screening; proteome analysis;
 gene therapy; antisense therapy; genotyping; transgenic animal; knock in;
 disease model; toxicological testing; transcript imaging;
 transcription factor; gene; ss.

OS Homo sapiens.

PN WC0200297031-A2.

ED 05-DEC-2002.

PF 27-MAR-2002; 2002WC-US010056.

XX 28-MAR-2001; 2001US-0279619P.
 PR 29-MAR-2001; 2001US-0280067P.
 PR 29-MAR-2001; 2001US-0280068P.
 PR 15-MAY-2001; 2001US-0291280P.
 PR 17-MAY-2001; 2001US-0291829P.
 PR 17-MAY-2001; 2001US-0291849P.
 PR 19-JUN-2001; 2001US-0299428P.
 PR 20-JUN-2001; 2001US-029976P.
 PR 20-JUN-2001; 2001US-030001P.

XX (INCY-) INCYTE GENOMICS INC.

XX Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;
 PI Dufour GE, Hillman JL, Yu JY, Tuason O, Yip PS, Amehy SR;
 PI Peralta CH, Dean TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstein EH;
 PI Flores V, Marwaha R, Lo A, Lan R, Urahsa ME;
 DR WPI; 2003-129518/12.
 DR F-PSDB; ABR41360.

XX Novel human diagnostic and therapeutic polypeptide useful for identifying
 PT test compound which specifically binds to a polypeptide encoded by human
 PI diagnostic and therapeutic polynucleotide, and to induce antibodies.
 XX

PS Claim 2; SEQ ID NO 221; 591bp; English.
XX The invention relates to novel human diagnostic and therapeutic
CC polynucleotides designated dithp (ACC46080-ACC6749) and to their encoded
CC proteins (DITHP; ABR41136-ABR41812). The invention also relates to
CC polynucleotide sequences at least 90% identical to the dithp cDNA
CC sequences of the invention; recombinant vectors, host cells and
CC transgenic organisms comprising a dithp nucleic acid sequence; the
CC recombinant production of DITHP proteins; antibodies specific for DITHP
CC proteins; microarrays comprising dithp nucleic acid sequences; methods of
CC detecting dithp nucleotide and protein sequences; methods of screening
CC for compounds which specifically bind a DITHP protein; and methods of
CC assessing the toxicity of test compounds using a dithp hybridisation
CC probe. Dithp nucleic acid sequences and DITHP proteins may be used in the
CC diagnosis of a wide variety of conditions including cancer and other cell
CC proliferative disorders; autoimmune or inflammatory disorders; bacterial,
CC viral, fungal or parasitic infections; hormonal disorders; metabolic
CC disorders; neurological disorders; gastrointestinal disorders; transport
CC disorders; and connective tissue disorders. They may also be used to
CC screen for modulators of protein activity or gene expression. DITHP
CC proteins can additionally be used in analysis of the proteome of a tissue
CC or cell type and to induce antibodies. The dithp nucleic acids are
CC additionally useful in somatic or germline gene therapy of the disorders
CC mentioned above, as a source of antisense sequences, as a source of
CC probes and primers, in genotyping and identification of individuals, in
CC the generation of transgenic animal models of human disease or knock in
CC humanised animals, in toxicological testing, and in transcript imaging.
CC The present sequence represents a dithp cDNA encoding a DITHP protein
CC which has transcription factor activity. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_dct_sequences
XX
SQ Sequence 3372 BP; 723 A; 947 C; 959 G; 743 T; 0 U; 0 Other;

Query Match 72.3%; Score 870.2; DB 8; Length 3372;
Best Local Similarity 99.3%; Pred. No. 2.2e-226;
Matches 905; Conservative 0; Mismatches 3; Indels 3; Gaps 3;

QY 295 CATTGACGAGTCACTGAGC-GGACTTCTTTGTTTCTTTCTTTGGGACACTCTGG 353
DB 2673 CTTGGCAGGTCACTGTAGCGGAGCTTTTGGTTTCTTTCTTTGGGACACTCTGG 2614
QY 354 ACTCACTCCCGACGATGAAGGGCGTGAAGCGCGGTGCTACGAGGGGGTGTGT 413
DB 2613 ACTCACTCCCGACGATGAAGGGCGTGAAGCGCGGTGCTACGAGGGGGTGTGT 2554
QY 414 GCCTGCGGAAGCGAGTCTGAGCATGCGCCGGGGCGAGGAAAGGCGCGAGCTGAGG 473
DB 2553 GCCTGCGGAAGCGAGTCTGAGCATGCGCCGGGGCGAGGAAAGGCGCGAGCTGAGG 2494
QY 474 AGCCGCTGAGCTTGTGACGACATGAACCACTGCTACTCCGCTGCGGGAAGTGGTAC 533
DB 2493 AGCCGCTGAGCTTGTGACGACATGAACCACTGCTACTCCGCTGCGGGAAGTGGTAC 2434
QY 534 CCGGAGTCCCGAGAGGCACTCAAGCTTAAGCCAGGTGAATCTTAACGCGCATCGACT 593
DB 2433 CCGGAGTCCCGAGAGGCACTCAAGCTTAAGCCAGGTGAATCTTAACGCGCATCGACT 2374
QY 594 ACATTCTGACCTGACGAGTAGTCTGAGCGAGCGAGCCCTGGAACCCCTGATGGCCCC 653
DB 2373 ACATTCTGACCTGACGAGTAGTCTGAGCGAGCGAGCCCTGGAACCCCTGATGGCCCC 2314
QY 654 ACATTCTGACCTGACGAGCGAGCTGCTCCGGAACCTTGTCACTTCCAAACGACAAAGGA 713
DB 2313 ACATTCTGACCTGACGAGCGAGCTGCTCCGGAACCTTGTCACTTCCAAACGACAAAGGA 2254
QY 714 GCTTTTGGCACTGACTCGGCGGTCTCTTCAACCTTCCAAAGCAGGTCTGCGCCCT 773
DB 2253 GCTTTTGGCACTGACTCGGCGGTCTCTTCAACCTTCCAAAGCAGGTCTGCGCCCT 2194
QY 774 TCTGCTGGAAGCCCGGAAAGCTTCTGCTCCGGAAGCGGACGAGGATGGGCCCA 833

DB 2193 TCTGCTGGAAGCCCGGAAAGCTTCTGCTCCGGAAGCGGACGAGGATGGGCCCA 2134
QY 834 CTTGCGCCCTGCGCACTTGAATCCAAATCCCTTCTTGAAGACTTAACTGGTCTGAG 893
DB 2133 CTTGCGCCCTGCGCACTTGAATCCAAATCCCTTCTTGAAGACTTAACTGGTCTGAG 2074
QY 894 GAGCGAAGACTGTGAATCTTGAAGCTGAGAGGCGAGAGCTAGCTTGGCCACCAAGCTGG 953
DB 2073 GAGCGAAGACTGTGAATCTTGAAGCTGAGAGGCGAGAGCTAGCTTGGCCACCAAGCTGG 2014
QY 954 GCGAGCTACCCCTGCTCCACCCCAACCCCAAGTTCTTAAGTCTTTTGAAGCGTGAAG 1013
DB 2013 GCGAGCTACCCCTGCTCCACCCCAACCCCAAGTTCTTAAGTCTTTTGAAGCGTGAAG 1954
QY 1014 TGTGGAAGAGTGTGCTGCTCCAAATGATCCAAAGGGGGGCGAGAGCTGTCTTGG 1073
DB 1953 TGTGGAAGAGTGTGCTGCTCCAAATGATCCAAAGGGGGGCGAGAGCTGTCTTGG 1894
QY 1074 TCTCCTTGAAGAAAGTCTGCTGCTGCTGATTTATGAATCTATATATAG-GTATATAGGT 1132
DB 1893 TCTCCTTGAAGAAAGTCTGCTGCTGCTGATTTATGAATCTATATATAGAGTATATAGGT 1834
QY 1133 TTTGTACCTTTTATACAGGAAAGTGAATCTTCTGTATCAATGCGATGTATATTAACCTTT 1192
DB 1833 TTTGTACCTTTTATACAGGAAAGTGAATCTTCTGTATCAATGCGATGTATATTAACCTTT 1775
QY 1193 TTTATTAAGTT 1203
DB 1774 TTTATTAAGTT 1764

RESULT 7
AAQ44245
ID AAQ44245 standard; cDNA; 982 BP.
XX
AC AAQ44245;
XX
DT 25-MAR-2003 (revised)
DT 23-NOV-1993 (first entry)
XX
DE HEIR-1 gene.
XX
KW Neuroblastoma; helix-loop-helix; allele; tumour; hepatoma; N-myc;
XX deletion; lp36.2-p36.1; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT 37..483
FT CDS
FT FT /*tag= b
FT /*label= HEIR-1
FT /*note= "Claim 1; Page 48"
FT CDS 124..483
FT FT /*tag= a
FT /*tag= g
FT /*tag= d
FT /*note= "ATTTA-sequence"
FT FT 971..976
FT FT /*tag= c
XX
PN MO9313205-A1.
XX
PD 08-JUL-1993.
XX
PF 19-DEC-1992; 92MO-BP002962.
XX
PR 23-DEC-1991; 91AT-00002559.
XX
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
PA (GETH) GENENTECH INC.
XX
PI Elmler W, Weich A;

DR WPI; 1993-227321/28.
XX P-PSDB; AAR38910.
PT Human DNA mapped in neuroblastoma consensus deletion region for gene
PT regulator - comprises nucleic acid sequence encoding specific aminoacid
PT helix loop helix protein for antibodies, for diagnosing pathological
PT conditions e.g. hepatoma.
XX
PS Disclosure; Page 41-42; 67pp; German.
XX
CC The gene is situated in the region of the neuroblastoma consensus
CC deletion 1p36.2-p36.1 and codes for a helix-loop-helix protein with the
CC designation HEIR-1. The gene is affected significantly by allelic tumour
CC deletions in neuroblastomas and correlates inversely both with N-myc
CC overexpression in tumours and with N-myc expression in normal
CC development. The cDNA and antibodies coding for HEIR-1 are used for the
CC diagnosis of pathological conditions associated with aberrations in the
CC region of the neuroblastoma consensus deletion. (Updated on 25-MAR-2003
CC to correct PN field.)
XX
SQ Sequence 982 BP; 211 A; 290 C; 263 G; 218 T; 0 U; 0 Other;

Query Match 71.2%; Score 856.2; DB 2; Length 982;
Best Local Similarity 97.7%; Pred. No. 8.6e-223;
Matches 900; Conservative 0; Mismatches 18; Indels 3; Gaps 3;

QY 284 GAGCGTGGCGCGCTTGGAGGTCAGTGAAGGACTTCTTTGGTTCTTTCTCTTGGG 343
DB 40 GATCTGTCAACAGCGGAACTCAAGCACTCACTTTTGGTTTCTTTCTTGGG 99
QY 344 GCACTTGTGACTCACTCTCCCAAGATGAAAGCGCTGAGCGCGCTGCTACGAG 403
DB 100 GCACTTGTGACTCACTCTCCCAAGATGAAAGCGCTGAGCGCGCTGCTACGAG 159
QY 404 GCGGTGTGCTGCTGTGCGAAGCGAGTGGCCATGCGCCGGGCGGAGGAGGCGCG 463
DB 160 GCGGTGTGCTGCTGTGCGAAGCGAGTGGCCATGCGCCGGGCGGAGGAGGCGCG 219
QY 464 GCACTGAGGAGCGCGCTGAGCTTGTGAGAGATGAAACCACTGTACTCCGCGCTGCG 523
DB 220 GCACTGAGGAGCGCGCTGAGCTTGTGAGAGATGAAACCACTGTACTCCGCGCTGCG 279
QY 524 GAACCTGGTACCGGAGTCCCGAGGCACTACAGCTTACAGGAGTGAATCTTCAAGGCG 583
DB 280 GAACCTGGTACCGGAGTCCCGAGGCACTACAGCTTACAGGAGTGAATCTTCAAGGCG 339
QY 584 GTTCATGACTAATTCGACCTGACGATGATCTTGCGGAGCGAGCCCTGGAACCCCT 643
DB 340 GTTCATGACTAATTCGACCTGACGATGATCTTGCGGAGCGAGCCCTGGAACCCCT 399
QY 644 GATGCGCCCGACCTTCCCATCGAGAGCGAGCTGCTCGGAACTTGTATCTCCAC 703
DB 400 GATGCGCCCGACCTTCCCATCGAGAGCGAGCTGCTCGGAACTTGTATCTCCAC 459
QY 704 GACAAAGAGAGCTTTTGCACAGCTCGGCGGTGCTCGAACCTCCGAAACGAGGTGC 763
DB 460 GACAAAGAGAGCTTTTGCACAGCTCGGCGGTGCTCGAACCTCCGAAACGAGGTGC 519
QY 764 TGGCGCCGCTTGTGCTGAGAGCCCGGGAACCTCTCTGCGGAGCGAGCGAGGGA 823
DB 520 TGGCGCCGCTTGTGCTGAGAGCCCGGGAACCTCTCTGCGGAGCGAGCGAGGGA 579
QY 824 TGGCGCCCGACCTTGGCCGCACTTGAATTCACCAATCCCTTCTGAGACTTAAAC 883
DB 580 TGGCGCCCGACCTTGGCCGCACTTGAATTCACCAATCCCTTCTGAGACTTGAAC 639
QY 884 TGGTCTCTAGAGCGAAGAGCTGTGAATTTGAGCTGAAAGCGAGCTAGCTTGGC 943
DB 640 TGGTCTCTAGAGCGAAGAGCTGTGAATTTGAGCTGAAAGCGAGCTAGCTTGGC 699
QY 944 CACGAGCTGGGCGAGCTGACCTGCTCCACACCCCAAGTTCTTAAGTCTTTTCA 1003
DB 700 CACGAGCTGGGCGAGCTGACCTGCTCCACACCCCA-CGCCAAGTTCTTAAGTCTTTTCA 758

QY 1004 AGCGTGAAGTGTGGAAGAGAGTGGCTCTCCAAACTATGCCAAGCGCGGAGAGCT 1063
DB 759 AGCGTGAAGTGTGGAAGAGAGTGGCTCTCCAAACTATGCCAAGCGCGGAGAGCT 818
QY 1064 GGTCTTGTGCTCTCTTGGAGAAAGTTCTGTGCGCTGATTTATGAATCTATATAG- 1122
DB 819 GGTCTTGTGCTCTCTTGGAGAAAGTTCTGTGCGCTGATTTATGAATCTATATAG 878
QY 1123 GATATAGTGTGACTTTTATACAGGAGGATGACTTGTGAACATGCGATGAT 1182
DB 879 GATATAGTGTGACTTTTATCA-GAAGGTGACTTGTGTAACAATGCGATGAT 937
QY 1183 ATTAACTTTTATATAAGTT 1203
DB 938 ATTAACTTTTATATAAGTT 958
RESULT 8
AB08114
ID AB08114 standard; cDNA; 982 BP.
XX
AC AB08114;
XX
DT 18-SEP-2002 (first entry)
XX
DE Human osteoblast differentiation related cDNA SEQ ID NO 21.
XX
KW Human, osteoblast; stem cell differentiation; bone tissue deposition;
KW osteoporosis; osteopathic; ss.
XX
OS Homo sapiens.
XX
EN W0200250301-A2.
XX
PD 27-JUN-2002.
XX
PF 18-DEC-2001; 2001MO-US048276.
XX
PR 18-DEC-2000; 2000US-0255882P.
PR 24-APR-2001; 2001US-0285691P.
XX
PA (GENE-) GENE LOGIC INC.
PA (PROC) PROCTER & GAMBLE CO.
XX
PI Ji D, Axelrod DW, Cook JS, Jalawal N, Einstein R, Houghton A;
PI Wertz L;
XX
DR WPI; 2002-557663/59.
XX
PT Use of genes and their expression profiles associated with osteoblast
PT differentiation for screening modulators bone formation, for diagnosing
PT or treating e.g. osteoporosis, or as markers for the differentiation
PT process.
XX
PS Claim 1; SEQ ID NO 21; 78bp + Sequence Listing; English.
XX
CC The invention relates to genes and their expression profiles are used
CC for: (a) screening modulators of precursor stem cell differentiation into
CC osteoblasts, or bone tissue deposition; (b) diagnosing abnormal
CC deposition of bone tissue, abnormal rate of osteoblast formation or
CC osteoporosis; or (c) treating or monitoring treatment of the conditions
CC cited in (b), or monitoring the progression of bone tissue deposition.
CC Specific conditions include postmenopausal osteoporosis, glucocorticoid
CC osteoporosis or male osteoporosis, osteopenia, osteodystrophy, drug-
CC induced abnormalities in bone formation or bone loss, conditions that
CC involve altered bone metabolism (e.g. idiopathic juvenile osteoporosis),
CC skeletal disease linked to breast cancer, mastocytosis, Fanconi syndrome
CC or fibrous dysplasia. The present sequence is that of an osteoblast
CC differentiation associated cDNA marker of the invention. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 982 BP; 211 A; 290 C; 263 G; 218 T; 0 U; 0 Other;
 SQ

Query Match 71.2%; Score 856.2; DB 6; Length 982;
 Best Local Similarity 97.7%; Pred. No. 8.6e-223;
 Matches 900; Conservative 0; Mismatches 18; Indels 3; Gaps 3;

```

OY 284 GAGCGGCGCGGCTTGACAGTCACTGTAGCGGACTTCTTTGGTTTCTTTCTTTGGG 343
DB 40 GATCTTGACCAACGGGAACTTCAACGACCTCACTTCTTTGTTTCTTTCTTTGGG 99
OY 344 GCACCTTGAGTCACTCCCGACATGAAAGCGCTGAGCCCGGTGCGCGCTGTACGAG 403
DB 100 GCACTCTGAGTCACTCCCGACATGAAAGCGCTGAGCCCGGTGCGCGCTGTACGAG 159
OY 404 GCGGTGTGCTGCTCTTGGAAAGCACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 463
DB 160 GCGGTGTGCTGCTCTTGGAAAGCACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 219
OY 464 GCAGCTGAGGAGCGCGCTGAGCTTGTGAGCGACATGAAACCACTGCTACCTCCGCTGCGG 523
DB 220 GCACTGAGAGAGCCCGTGAAGCTTGTGCTGAGCAATGAAACCACTGCTACCTCCGCTGCGG 279
OY 524 GAACTGTGTAACCGGAGTCCCGAGAGCACTGAGCTTGAAGCAAGTGAATCTTACAGCGC 583
DB 280 GAACTGTGTAACCGGAGTCCCGAGAGCACTGAGCTTGAAGCAAGTGAATCTTACAGCGC 339
OY 584 GTCACTGATCACTTCTGCACTTGTGAGTCTTGGCGGAGCCAGCCCTTGGACCCCT 643
DB 340 GTCACTGATCACTTCTGCACTTGTGAGTCTTGGCGGAGCCAGCCCTTGGACCCCT 399
OY 644 GATGCGCCCGACCTTCCCATTCAGACAGCGGAGCTGCTGCGGAACTTGTCTCTCCAC 703
DB 400 GATGCGCCCGACCTTCCCATTCAGACAGCGGAGCTGCTGCGGAACTTGTCTCTCCAC 459
OY 704 GACAAAGAGCTTGTGCACTGAGTCCGCGCTGTCTGACACCTTCCAGAAAGCAGAGTGC 763
DB 460 GACAAAGAGCTTGTGCACTGAGTCCGCGCTGTCTGACACCTTCCAGAAAGCAGAGTGC 519
OY 764 TGGCGCCCGCTTGTGCTGAGGAGCCCGGAGAACTTCTTCTGCGGAAAGCGGAGGGA 823
DB 520 TGGCGCCCGCTTGTGCTGAGGAGCCCGGAGAACTTCTTCTGCGGAAAGCGGAGGGA 579
OY 824 TGGCGCCCGACCTTGTGCGCCCTGCGCACTTGAACCTTCAACCAATCCCTTCTGAGACTTAAC 883
DB 580 TGGCGCCCGACCTTGTGCGCCCTGCGCACTTGAACCTTCAACCAATCCCTTCTGAGACTTAAC 639
OY 884 TGGTCTCAAGAGAGGAGCTGTGAACCTTGTAGCTGAAAGAGCAAGCTAGCTTGGC 943
DB 640 TGGTCTCAAGAGAGGAGCTGTGAACCTTGTAGCTGAAAGAGCAAGCTAGCTTGGC 699
OY 944 CACGAGCTGAGGAGCTGACCTGTCTCCAGCCCAACCCCAAGTTCTTAAGTCTTTTNG 1003
DB 700 CACGAGCTGAGGAGCTGACCTGTCTCCAGCCCAACCCCAAGTTCTTAAGTCTTTTNG 758
OY 1004 AGCGTGAAGTGTGAAAGAGTGTGCTCTTCAAACTTGTCCAAAGGCGGCGGCGAGAGT 1063
DB 759 AGCGTGAAGTGTGAAAGAGTGTGCTCTTCAAACTTGTCCAAAGGCGGCGGCGAGAGT 818
OY 1064 GGTCTTCTGAGTCTCTTGTGAGAAAGTTCTGTGCGCTGATTTATGAATCTTATATAG- 1122
DB 819 GGTCTTCTGAGTCTCTTGTGAGAAAGTTCTGTGCGCTGATTTATGAATCTTATATAG 878
OY 1123 GTATATAGTGTGTAACCTTTTATACAGGAAGTGTACTTGTATACAAATGCAATGAT 1182
DB 879 GTATATAGTGTGTAACCTTTTATACAGGAAGTGTACTTGTATACAAATGCAATGAT 937
OY 1183 ATTAATCTTTTATATAAGTT 1203
DB 938 ATTAATCTTTTATATAAGTT 958

```

RESULT 9

ACC46763
 ID ACC46763 standard; cDNA; 982 BP.

XX AC ACC46763;
 AC ACC46763;
 DT 05-JUN-2003 (first entry)

XX Human COPD related protein encoding cDNA SEQ ID NO:14.

XX Human; chronic obstructive pulmonary disease; COPD; chronic lung disease;
 KW gene; 98.

XX Homo sapiens.

XX WO200297127-A2.

XX PD 05-DEC-2002.

XX PF 28-MAY-2002; 2002MO-EP005835.

XX PR 31-MAY-2001; 2001GB-00013266.

XX PA (FARB) BAYER AG.

XX Oellers N, Gehrman M, Kallabis H, Hall R, Schulze T, Kroegel C;

XX WPI; 2003-140492/13.

XX DR P-PSDB; ABP96792.

XX PT Predicting, diagnosing or prognosing chronic lung disease, by detecting a
 PS chronic obstructive pulmonary disease (COPD) gene in a biological sample.

XX Claim 8; Page 96-97; 214pp; English.

XX The present invention describes a method for predicting, diagnosing or
 CC prognosing chronic lung disease by detecting a chronic obstructive

CC pulmonary disease (COPD) gene related polynucleotide (see ACC46750 to
 CC ACC46777, which encode the COPD related proteins in ABP96779 to

CC ABP96806). The method is useful for predicting, diagnosing or prognosing
 CC chronic lung disease in a biological sample. The COPD genes and proteins

CC encoded by them from the present invention (I) can be used for treating
 CC or preventing chronic lung disease in a mammal. (I) can be used in an

CC animal model for determining the efficacy, toxicity, or side effects of
 CC treatment with (I), and determining the mechanism of action of (I).

CC ACC46778 to ACC46903 represent COPD related PCR primers and probes used
 CC in an example from the present invention

XX Sequence 982 BP; 211 A; 290 C; 263 G; 218 T; 0 U; 0 Other;

XX Query Match 71.2%; Score 856.2; DB 10; Length 982;

XX Best Local Similarity 97.7%; Pred. No. 8.6e-223;
 XX Matches 900; Conservative 0; Mismatches 18; Indels 3; Gaps 3;

OY 284 GAGCGTGGCGCGGTTGACAGTCACTGTAGCGGACTTCTTTGGTTTCTTTCTTTGGG 343

DB 40 GATCTTGACCAACGGGAACTTCAACGACCTCACTTCTTTGTTTCTTTCTTTGGG 99

OY 344 GCACCTTGAGTCACTCCCGACATGAAAGCGCTGAGCCCGGTGCGCGCTGTACGAG 403

DB 100 GCACTCTGAGTCACTCCCGACATGAAAGCGCTGAGCCCGGTGCGCGCTGTACGAG 159

OY 404 GCGGTGTGCTGCTCTTGGAAAGCACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 463

DB 160 GCGGTGTGCTGCTCTTGGAAAGCACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 219

OY 464 GCAGCTGAGGAGCGCGCTGAGCTTGTGAGCGACATGAAACCACTGCTACCTCCGCTGCGG 523

DB 220 GCACTGAGGAGCGCGCTGAGCTTGTGAGCGACATGAAACCACTGCTACCTCCGCTGCGG 279

OY 524 GAACTGTGTAACCGGAGTCCCGAGAGCACTGAGCTTGAAGCAAGTGAATCTTACAGCGC 583

DB 280 GAACTGTGTAACCGGAGTCCCGAGAGCACTGAGCTTGAAGCAAGTGAATCTTACAGCGC 339

QY 584 GTGATGAGTGAATCTGAGAGGAGTCTGGCCGAGGAGCCGCTTGAGACCCCT 643
DB 340 GTGATGAGTGAATCTGAGAGGAGTCTGGCCGAGGAGCCGCTTGAGACCCCT 399
QY 644 GATGGCCCGACCTTCCATCCAGACAGCCGAGTCTGGCCGAGGAGCTTGATCTCCAC 703
DB 400 GATGGCCCGACCTTCCATCCAGACAGCCGAGTCTGGCCGAGGAGCTTGATCTCCAC 459
QY 704 GACAAAAGAGCTTTTGACAGTCTGGCCGAGTCTGGCCGAGGAGCTTGATCTCCAC 763
DB 460 GACAAAAGAGCTTTTGACAGTCTGGCCGAGTCTGGCCGAGGAGCTTGATCTCCAC 519
QY 764 TGGCCCGCTTCTGCTGAGAGCCCGGAGACCTTCTGCGAGGAGCCGAGGAGGAG 823
DB 520 TGGCCCGCTTCTGCTGAGAGCCCGGAGACCTTCTGCGAGGAGCCGAGGAGGAG 579
QY 824 TGGCCCGCTTCTGCTGAGAGCCCGGAGACCTTCTGCGAGGAGCCGAGGAGGAG 883
DB 580 TGGCCCGCTTCTGCTGAGAGCCCGGAGACCTTCTGCGAGGAGCCGAGGAGGAG 639
QY 884 TGGTGTCTGAGAGGAGAGAGCTGTAAGTCTGTAAGAGAGAGAGAGAGTCTGAG 943
DB 640 TGGTGTCTGAGAGGAGAGAGCTGTAAGTCTGTAAGAGAGAGAGAGTCTGAG 699
QY 944 CACAGCTGGGCGGAGCTGACCTGCTCCACCCGAGCCGAGGAGTCTGAGTCTTCA 1003
DB 700 CACAGCTGGGCGGAGCTGACCTGCTCCACCCGAGCCGAGGAGTCTGAGTCTTCA 758
QY 1004 AGCGTGGAGGAGTGGAGAGAGTGGCTGCTCCAACTGAGCCGAGGAGGAGGAGT 1063
DB 759 AGCGTGGAGGAGTGGAGAGAGTGGCTGCTCCAACTGAGCCGAGGAGGAGGAGT 818
QY 1064 GGTCTTCTGCTGCTGCTGAGAGAGGTTCTGAGCCCTGATTTATGAG- 1122
DB 819 GGTCTTCTGCTGCTGCTGAGAGAGGTTCTGAGCCCTGATTTATGAG- 878
QY 1123 GATATAGAGTGTGACCTTTTTCAGAGGAGTCTGTAAGAGTCTGTAAGTCTGTA 1182
DB 879 GATATAGAGTGTGACCTTTTTCAGAGGAGTCTGTAAGAGTCTGTAAGTCTGTA 937
QY 1183 ATTAACTTTTATTAAGTT 1203
DB 938 ATTAACTTTTATTAAGTT 958
RESULT 10
AD124462
ID AD124462 standard, cDNA, 982 BP.
AC AD124462;
AD 15-APR-2004 (first entry)
DE Human modifier of Chk1 (MCHK) encoding cDNA SEQ ID NO:12.
KW Chk1 pathway modulating agent; modifier of Chk1; MCHK; cytostatic;
KW gene therapy; cancer; human; gene; se.
OS Homo sapiens.
XX WO2004004785-A1.
XX 15-JAN-2004.
XX 09-JUL-2003; 2003WO-US021379.
XX 10-JUL-2002; 2002US-0394845P.
XX 16-SEP-2002; 2002US-0410986P.
XX (EXEL-) EXELIXIS INC.
XX Francis-Lang H, Roche S, Joo DM, Nicoll M, Hai B, Zhang H;
PI Lichteig K, Amundsen CD, Jin Y, Adamkewicz JT, Plact DM;

PI Hammonds RG;
XX WPI: 2004-083465/08.
DR P-PSDB; AD124512.
XX
XX Identifying a candidate Chk1 pathway modulating agent for treating e.g.,
PT cancer, comprises contacting an assay system comprising a MCHK
PT polypeptide or nucleic acid with a test agent and detecting a test agent-
PT biased activity.
XX
PS Example; SEQ ID NO 12; 266bp; English.
XX
CC The present invention describes a method for identifying a candidate Chk1
CC pathway modulating agent. The method comprises: (a) providing an assay
CC system comprising a modifier of Chk1 (MCHK) polypeptide or nucleic acid;
CC (b) contacting the system with a test agent, where the system provides a
CC reference activity except in the presence of the test agent; and (c)
CC detecting a test agent-biased activity, and a difference between the test
CC agent-biased activity and the reference activity. Also described: (1) a
CC method for modulating Chk1 pathway of a cell; (2) a method for diagnosing
CC Chk1 pathway in a mammalian cell; and (3) a method for diagnosing a
CC disease in a patient. A MCHK sequence has cytostatic activity, and can be
CC used in gene therapy. The method is useful for identifying a candidate
CC Chk1 pathway-modulating agent for preparing a composition for diagnosing
CC or treating e.g., cancer. The present sequence encodes a human MCHK
CC protein, which is used in the exemplification of the present invention.
XX
SQ Sequence 982 BP; 211 A; 290 C; 263 G; 218 T; 0 U; 0 Other;
Query Match 71.2%; Score 856.2; DB 12; Length 982;
Best Local Similarity 97.7%; Pred. No. 8, 6e-223;
Matches 900; Conservative 0; Mismatches 18; Indels 3; Gaps 3;
QY 284 GAGGTGCGGCGCGTTCAGAGTCTGAGCGGAGTCTGAGTCTGAGTCTGAGTCTGAG 343
DB 40 GATCTGAGCAGCAGGAGACCTACACACACTTCTTTGTTCTTCTTCTTCTTCTTCTT 99
QY 344 GCACCTTCTGAGTCTCTCCCGCAGATGAGGCGTCTGAGCGCGTCTGAGCAG 403
DB 100 GCACCTTCTGAGTCTCTCCCGCAGATGAGGCGTCTGAGCGCGTCTGAGCAG 159
QY 404 GCGGTGTGCTGCTGCTGAGAGAGTCTGAGCGCGTCTGAGCGCGTCTGAGCG 463
DB 160 GCGGTGTGCTGCTGCTGAGAGAGTCTGAGCGCGTCTGAGCGCGTCTGAGCG 219
QY 464 GCAGCTGAGAGCGCGTCTGAGCGCGTCTGAGCGCGTCTGAGCGCGTCTGAGCG 523
DB 220 GCAGCTGAGAGCGCGTCTGAGCGCGTCTGAGCGCGTCTGAGCGCGTCTGAGCG 279
QY 524 GAACTGTGACCGGAGAGTCTGAGCGCGTCTGAGCGCGTCTGAGCGCGTCTGAGCG 583
DB 280 GAACTGTGACCGGAGAGTCTGAGCGCGTCTGAGCGCGTCTGAGCGCGTCTGAGCG 339
QY 584 GTGATGAGTGAATCTGAGAGGAGTCTGAGCGCGTCTGAGCGCGTCTGAGCGCGT 643
DB 340 GTGATGAGTGAATCTGAGAGGAGTCTGAGCGCGTCTGAGCGCGTCTGAGCGCGT 399
QY 644 GATGGCCCGACCTTCCATCCAGACAGCCGAGTCTGGCCGAGGAGCTTGATCTCCAC 703
DB 400 GATGGCCCGACCTTCCATCCAGACAGCCGAGTCTGGCCGAGGAGCTTGATCTCCAC 459
QY 704 GACAAAAGAGCTTTTGACAGTCTGGCCGAGTCTGGCCGAGGAGCTTGATCTCCAC 763
DB 460 GACAAAAGAGCTTTTGACAGTCTGGCCGAGTCTGGCCGAGGAGCTTGATCTCCAC 519
QY 764 TGGCCCGCTTCTGCTGAGAGCCCGGAGACCTTCTGCGAGGAGCCGAGGAGGAG 823
DB 520 TGGCCCGCTTCTGCTGAGAGCCCGGAGACCTTCTGCGAGGAGCCGAGGAGGAG 579
QY 824 TGGCCCGCTTCTGCTGAGAGCCCGGAGACCTTCTGCGAGGAGCCGAGGAGGAG 883
DB 580 TGGCCCGCTTCTGCTGAGAGCCCGGAGACCTTCTGCGAGGAGCCGAGGAGGAG 639

QY 884 TGGTCTCAGAGCGAGAGCTGTGAACTTGTAGCTGAGGAGCCAGAGCTAGCTCTG9C 943
DB 640 TGGTCTCAGAGCGAGAGCTGTGAACTTGTAGCTGAGGAGCCAGAGCTAGCTCTG9C 699
QY 944 CACGAGCTGGGCGAGAGCTGACCTGCTCCACCCACCCCAAGTTCTAGGTCTTTTCAG 1003
DB 700 CACGAGCTGGGCGAGAGCTGACCTGCTCCACCCCAAGTTCTAGGTCTTTTCAG 758
QY 1004 AGCGTGAAGGTGTGAGAGAGTGTGCTCTCCAACTATGCCAGGCGCGGAGAGCT 1063
DB 759 AGCGTGAAGGTGTGAGAGAGTGTGCTCTCCAACTATGCCAGGCGCGGAGAGCT 818
QY 1064 GGTCTTCTGCTCTCTGAGAGAGTGTGCTGCTCCAACTATGCCAGGCGCGGAGAGCT 1122
DB 819 GGTCTTCTGCTCTCTGAGAGAGTGTGCTGCTCCAACTATGCCAGGCGCGGAGAGCT 878
QY 1123 GTATATAGGTTTGTACCTTTTTCACAGGAGGTGATCTTGTAACTGATGAT 1182
DB 879 GTATATAGGTTTGTACCTTTTTCACAGGAGGTGATCTTGTAACTGATGAT 937
QY 1183 ATTAACCTTTTATATAAGTT 1203
DB 938 ATTAACCTTTTATATAAGTT 958
RESULT 11
ADL82868 standard; cDNA, 982 BP.
XX ADL82868;
XX
XX 17-JUN-2004 (first entry)
XX
DE Human PRO37957 cDNA, SEQ ID 70.
XX
XX Immunosuppressive; Cytostatic; Antiarthritic; Antirheumatic; Antianemic;
XX Anti-allergic; Muscular; Neuroprotective; Nephroretropic; Antiinflammatory;
XX Gene Therapy; PRO; B cell related disorder; cancer;
XX Immune-mediated inflammatory disease; human; gene; ss.
XX
XX Homo sapiens.
XX
XX WO2004024097-A2.
XX
XX 25-MAR-2004.
XX
XX 15-SEP-2003; 2003WO-US029097.
XX
XX 16-SEP-2002; 2002US-0411392P.
XX
XX (GETH) GENENTECH INC.
XX
XX Chiu H, Clark H, Dennis K, Fong S, Schoenfeld JR, Wood WI,
XX Wu TD;
XX
XX MPI. 2004-329389/30.
XX P-PSDB: ADL82869.
XX
XX
XX New PRO polypeptide, useful for diagnosing and treating a B cell related
XX disorder, e.g. Burkitt's lymphoma, rheumatoid arthritis, autoimmune
XX mediated hemolytic anemia, myasthenia gravis or ankylosing spondylitis.
XX
XX Claim 2; Fig 70; 695pp; English.
XX
XX
XX The present invention relates to PRO proteins and their coding sequences.
XX The PRO proteins are useful for diagnosing and treating a B cell related
XX disorder, e.g. X-linked infantile hypogammaglobulinemia, polyasaccharide
XX antigen unresponsiveness, selective iga deficiency, selective igh
XX deficiency, selective deficiency of iga subclasses, immunodeficiency with
XX hyper igm, transient hypogammaglobulinemia of infancy, Burkitt's
XX lymphoma, intermediate lymphoma, follicular lymphoma, type II
XX hypersensitivity, rheumatoid arthritis, autoimmune mediated haemolytic
XX anaemia, myasthenia gravis, hypoadrenocorticism, glomerulonephritis, or

CC ankylosing spondylitis. The PRO proteins are also useful for preparing a
CC medicament for treating a condition that is responsive to the PRO
CC protein, e.g. cancer or immune-mediated inflammatory diseases. The PRO
CC coding sequences are useful as hybridization probes in chromosome and
CC gene mapping, in preparing PRO proteins, or in generating transgenic
CC animals or knockout animals, which in turn are useful in the development
CC and screening of therapeutically useful reagents.
XX
SQ Sequence 982 BP, 211 A, 290 C, 263 G, 218 T, 0 U, 0 Other:
Query Match 71.2%; Score 856.2; DB 12; Length 982;
Best Local Similarity 97.7%; Pred. No. 8-6e-223;
Matches 900; Conservative 0; Mismatches 18; Indels 3; Gaps 3;
QY 284 GAGCGTGGCGCGGTTGCGAGGTGATGCGGACTTTCTTTTCTTTTCTTTTGGG 343
DB 40 GATCTCGACCAAGGGAAGCTCAGACCTCATTCTTTGTTTCTTTTCTTTTGGG 99
QY 344 GCACCTCGGACTGCTGCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 403
DB 100 GCACCTCGGACTGCTGCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 159
QY 404 GCGGTGCTGCTGCTGCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 463
DB 160 GCGGTGCTGCTGCTGCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 219
QY 464 GCGGTGCTGCTGCTGCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 523
DB 220 GCGGTGCTGCTGCTGCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 279
QY 524 GAGCTGTGACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 583
DB 280 GAGCTGTGACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 339
QY 584 GTCATGCACTACCTTCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 643
DB 340 GTCATGCACTACCTTCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 399
QY 644 GATGCGCCCACTTCCCAATCCAGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 703
DB 400 GATGCGCCCACTTCCCAATCCAGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 459
QY 704 GACAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 763
DB 460 GACAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 519
QY 764 TGGCGCCCGCTTCTGCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 823
DB 520 TGGCGCCCGCTTCTGCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 579
QY 824 TGGCGCCCACTTCCCAATCCAGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 883
DB 580 TGGCGCCCACTTCCCAATCCAGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 639
QY 884 TGGTCTCAGAGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 943
DB 640 TGGTCTCAGAGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 699
QY 944 CACGAGCTGGGCGAGAGCTGACCTGCTCCACCCACCCCAAGTTCTAGGTCTTTTCAG 1003
DB 700 CACGAGCTGGGCGAGAGCTGACCTGCTCCACCCCAAGTTCTAGGTCTTTTCAG 758
QY 1004 AGCGTGAAGGTGTGAGAGAGTGTGCTCTCCAACTATGCCAGGCGCGGAGAGCT 1063
DB 759 AGCGTGAAGGTGTGAGAGAGTGTGCTCTCCAACTATGCCAGGCGCGGAGAGCT 818
QY 1064 GGTCTTCTGCTCTCTGAGAGAGTGTGCTGCTCCAACTATGCCAGGCGCGGAGAGCT 1122
DB 819 GGTCTTCTGCTCTCTGAGAGAGTGTGCTGCTCCAACTATGCCAGGCGCGGAGAGCT 878
QY 1123 GTATATAGGTTTGTACCTTTTTCACAGGAGGTGATCTTGTAACTGATGAT 1182
DB 879 GTATATAGGTTTGTACCTTTTTCACAGGAGGTGATCTTGTAACTGATGAT 937

DR WPI; 2003-058567/05.

PT Novel isolated nucleic acid upregulated/downregulated in osteogenesis
PT useful for bone disease therapy in subject.

PS Claim 26; Page 151; 237pp; English.

CC The present invention relates to novel nucleotide sequences, which are
CC differentially expressed in models of osteogenesis upon being put in
CC contact with a stimulator of osteogenesis. The present sequence is one
CC such sequence. This sequence can be used for diagnosing osteoporosis/bone
CC diseases in a patient, promoting osteogenesis and/or preventing
CC osteoporosis/bone diseases. The present sequence encodes a transcription
CC factor or an orphan nuclear receptor

Sequence 2481 BP; 521 A; 662 C; 699 G; 599 T; 0 U; 0 other;

Query Match	Score	DB	Length
55.2%	663.8	8	2481

Best Local Similarity 99.7%; Pred. No. 3.5e-170;

Matches 665; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY	1	GATCTGGGGTGTGTGCGAGGAAAAAACCAATTCTGGAGTTAATGGTTTGAAGTATCT	60
Db	372	GATCTGGGGTGTGTGCGAGGAAAAAACCAAAATTCTGGAAGTTAAATGGTTTGAAGTATCT	431
OY	61	AAATCTTGTCTGGCGAGAGAGGCGCCGCTCTCCCGGTATACAGCGCTCTCATTTCTTGA	120
Db	432	AAATCTTGTCTGGCGAGAGAGGCGCCGCTCTCCCGGTATACAGCGCTCTCATTTCTTGA	491
OY	121	ATCCGGGCTCCGCGGTCTTTCGGCTCAGACCAGCCGAGAGGAAGCTGTTTGCAATTTAA	180
Db	492	ATCCGGGCTCCGCGGTCTTTCGGCTCAGACCAGCCGAGAGGAAGCTGTTTGCAATTTAA	551
OY	181	GCGGGCTGTGAACCGCCAGAGGCGCGGCGGGGCGGGGCGAGGCGGCAATTTGAAATAA	240
Db	552	GCGGGCTGTGAACCGCCAGAGGCGCGGCGGGGCGGGGCGAGGCGGCAATTTGAAATAA	611
OY	241	GAGGCGTCCCTTCCAGGCGAGGCTCTATAAGTACCGCGCGGCGAGCGGCGGGGTGC	300
Db	612	GAGGCGTCCCTTCCAGGCGAGGCTCTATAAGTACCGCGCGGCGAGCGGCGGGGTGC	671
OY	301	AGGTCACTGTAGCGGACTTCTTTTGGTTTTCTTCTTTTGGGGCACTCTGGACTCACT	360
Db	672	AGGTCACTGTAGCGGACTTCTTTTGGTTTTCTTCTTTTGGGGCACTCTGGACTCACT	731
OY	361	CCCCAGCATGAAGGCGCTGAGCCCGGTGCGCGGCTGTAAGAGCGGTGTGCTCTGTTC	420
Db	732	CCCCAGCATGAAGGCGCTGAGCCCGGTGCGCGGCTGTAAGAGCGGTGTGCTCTGTTC	791
OY	421	GGAAGCGACTCTGGGCAATCGCCCGGGGCGAGAGGAAGGGCCCGGCACTGAGAGCCGCT	480
Db	792	GGAAGCGACTCTGGGCAATCGCCCGGGGCGAGAGGAAGGGCCCGGCACTGAGAGCCGCT	851
OY	481	GAGCTTTCGGAAGCATGAACCACTGCTACTCCCGCTGCGGGAATGTTACCCGGAAGT	540
Db	852	GAGCTTTCGGAAGCATGAACCACTGCTACTCCCGCTGCGGGAATGTTACCCGGAAGT	911
OY	541	CCCGAGAGGCACTCAGCTTAGCCAGAGTGGAAATCTTACAGCGCGTCACTGACTATCT	600
Db	912	CCCGAGAGGCACTCAGCTTAGCCAGAGTGGAAATCTTACAGCGCGTCACTGACTATCT	971
OY	601	CGACTTGCAGGTAGTCTCTGGCCGAGCCAGCCCTCTGAGCCCTCTGATGGCCCCCACTTCC	660
Db	972	CGACTTGCAGGTAGTCTCTGGCCGAGCCAGCCCTCTGAGCCCTCTGATGGCCCCCACTTCC	1031
OY	661	CATCCAG 667	
Db	1032	CATCCAG 1038	

RESULT 14
ABQ88117/c
ID ABQ88117 standard; cDNA; 129722 BP.

XX ABQ88117;
AC

DT 18-SEP-2002 (first entry)

Human osteoblast differentiation related CDNA SEQ ID NO 24.

KM Human; osteoblast; stem cell differentiation; bone tissue deposition;
KM osteoporosis; osteopathic; ss.

OS Homo sapiens.

PN WO200250301-A2

PD 27-JUN-2002.

PF 18-DEC-2001; 2001WO-US048276.

PR 18-DEC-2000; 2000US-0255882P.

XX
XX
/ 22 21 20 19 18 17 16 15 14 13 12 11 10 9 8 7 6 5 4 3 2 1

PA (PROC) PROCTER & GAMBLE CO.

PI Ji D, Axelrod DW, Cook JS,

PI Mertz L;
....

WPI; 2002-557663/59.

PT Use of genes and the

PT or treating e.g. osteoporosis, or as markers for the differentiation PT process.

PS Claim 1; SEQ ID NO 24; 78bp + Sequence Listing; English.

CC The invention relates to genes and their expression profiles are used
CC for: (a) screening modulators of precursor stem cell differentiation into
CC osteoblasts, or bone tissue deposition; (b) diagnosing abnormal
CC deposition of bone tissue, abnormal rate of osteoblast formation or
CC osteoporosis; or (c) treating or monitoring treatment of the conditions
CC cited in (b), or monitoring the progression of bone tissue deposition.
CC Specific conditions include postmenopausal osteoporosis, glucocorticoid
CC osteoporosis or male osteoporosis, osteopenia, osteodystrophy, drug-
CC induced abnormalities in bone formation or bone loss, conditions that
CC involve altered bone metabolism (e.g. idiopathic juvenile osteoporosis),
CC skeletal disease linked to breast cancer, mastocytosis, Fanconi syndrome
CC or fibrous dysplasia. The present sequence is that of an osteoblast
CC differentiation associated cDNA marker of the invention. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 129722 BP; 33298 A; 32697 C; 31415 G; 32312 T; 0 U; 0 Other;

Query Match	Score	DB	Length
54.3%	652.8	6	129722

Best Local Similarity 99.6%; Pred. No. 1.7e-166;

Matches 665; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Qy	1	AATCGGGGCTCTGCAGAGAAAACAATTCTGGAAGTAAAGTTTGAGTGATCTT	60
Db	109558	GATCGGGGCTCTGCCAGAAAACAAATTCTGGAAGTAAATGCTTTGAGTGATTTT	1094599
Qy	61	AAATCTTGCTGGCGGAGAGGCCGCTCTCTCCCGGATCAGCGCTTCTCATTTCTTA	120
Db	109498	AAATCTTGCTGGCGGAGAGGCCGCTCTCTCCCGGATCAGCGCTTCTCATTTCTTTA	109439
Qy	121	ATCGCGGCTCCGGGCTCTTGCGGCTCAGACCGCGGAGGAAAGCTGTTCAATTAA	180
Db	109438	ATCGCGGCTCCGGGCTCTTGCGGCTCAGACCGCGGAGGAAAGCTGTTGCAATTAA	109379
Qy	181	GCGGCTGTGAACGCCACAGGCGCGGCGGAGCGGAGCGCGGCATTTTGAATAAA	240

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OM nucleic - nucleic search, using sw model

Run on: December 18, 2004, 15:14:56 / Search time 119.791 Seconds
(without alignments)
7138.064 Million cell updates/sec

Title: US-09-996-529a-5

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Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/pdata/1/lna/5B_COMB.seq:*
3: /cgn2_6/pdata/1/lna/6A_COMB.seq:*
4: /cgn2_6/pdata/1/lna/6B_COMB.seq:*
5: /cgn2_6/pdata/1/lna/PCROS_COMB.seq:*
6: /cgn2_6/pdata/1/lna/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	856.2	71.2	982	1	US-08-256-077-1 Sequence 1, Appl1
2	856.2	71.2	982	1	US-08-466-127-1 Sequence 1, Appl1
3	437.8	36.4	653	4	US-09-919-039-214 Sequence 214, App
4	360	29.9	360	1	US-08-256-077-3 Sequence 3, Appl1
5	360	29.9	360	1	US-08-466-127-3 Sequence 3, Appl1
6	306.4	25.5	446	1	US-08-256-077-5 Sequence 5, Appl1
7	306.4	25.5	446	1	US-08-466-127-5 Sequence 5, Appl1
8	198.4	16.5	255	4	US-09-513-999C-23008 Sequence 23008, A
9	75	6.2	926	1	US-08-151-391A-3 Sequence 3, Appl1
10	75	6.2	926	3	US-09-561-497-3 Sequence 3, Appl1
11	73.4	6.1	509	1	US-08-151-391A-1 Sequence 1, Appl1
12	70	5.8	4793	3	US-09-561-497-10 Sequence 10, Appl1
13	69	5.7	721	3	US-08-896-164-30 Sequence 30, Appl1
14	62.8	5.0	626	4	US-09-621-976-2005 Sequence 2005, Ap
15	47.6	4.2	1309	3	US-08-362-495-4 Sequence 4, Appl1
16	47.6	4.0	1309	3	US-09-408-508-4 Sequence 4, Appl1
17	43.6	3.6	1635	3	US-09-234-332-4 Sequence 4, Appl1
18	43.6	3.6	1635	4	US-09-702-705-1798 Sequence 1798, Ap
19	43.6	3.6	1635	4	US-09-736-457-1798 Sequence 1798, Ap
20	43.6	3.6	1635	4	US-09-671-325-1798 Sequence 1798, Ap
21	42	3.5	2175	4	US-09-252-991A-15144 Sequence 15144, A
22	42	3.5	2721	4	US-09-252-991A-15144 Sequence 15144, A
23	42	3.5	2781	4	US-09-252-991A-14482 Sequence 14482, A
24	41.8	3.5	846	4	US-09-252-991A-13245 Sequence 13245, A
25	41.8	3.5	879	4	US-09-252-991A-12714 Sequence 12714, A
26	41.8	3.5	1428	4	US-09-252-991A-12923 Sequence 12923, A
27	41.8	3.5	1455	4	US-09-252-991A-12561 Sequence 12561, A

28	40.6	3.4	703	4	US-09-799-451-19 Sequence 19, Appl
29	40.6	3.4	1287	4	US-09-799-451-469 Sequence 469, App
30	40.2	3.3	411	4	US-09-252-991A-14903 Sequence 14903, A
31	40.2	3.3	821	2	US-08-939-002A-15 Sequence 15, Appl
32	40.2	3.3	1436	3	US-09-199-637A-131 Sequence 131, App
33	40.2	3.3	3157	2	US-08-939-002A-1 Sequence 1, Appl1
34	39.6	3.3	1191	4	US-09-489-039A-5044 Sequence 5044, Ap
35	39.4	3.3	1572	4	US-09-252-991A-16430 Sequence 16430, A
36	39.4	3.3	1752	4	US-09-252-991A-16164 Sequence 16164, A
37	39	3.2	1248	4	US-09-724-797-23 Sequence 23, Appl
38	39	3.2	3348	4	US-09-799-451-302 Sequence 302, App
39	39	3.2	3511	4	US-09-799-451-456 Sequence 456, App
40	38.4	3.2	1245	4	US-09-252-991A-5535 Sequence 5535, Ap
41	38.2	3.2	1608	4	US-09-252-991A-8896 Sequence 8896, Ap
42	38.2	3.2	1504	4	US-09-252-991A-8091 Sequence 8091, Ap
43	38.2	3.2	1710	4	US-09-252-991A-9011 Sequence 9011, Ap
44	38.2	3.2	1920	4	US-09-252-991A-8999 Sequence 8999, Ap
45	37.6	3.1	277	2	US-08-690-011A-30 Sequence 30, Appl

ALIGNMENTS

RESULT 1
US-08-256-077-1
; Sequence 1, Application US/08256077
; Patent No. 5654188
; GENERAL INFORMATION:
; APPLICANT: Elimeier, Wilfried
; APPLICANT: Weith, Andreas
; TITLE OF INVENTION: Neuroblastoma-Associated Regulator Gene
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/256,077
; FILING DATE: 23-JUNE-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Emond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 0652.1360000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 982 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-256-077-1
Query Match 71.2%; Score 856.2; DB 1; Length 982;
Best Local Similarity 97.7%; Pred. No. 5.7e+231;
Matches 900; Conservative 0; Mismatches 16; Indels 3; Gaps 3;
QY 284 GAGCGTGGCGCGGCTTGCAGCTGACCTGTCAGGACTCTTTGTTCTTTCTTTGGG 343
DB 40 GATCTCTGACGACCGGAACTCTACGACCTCTCTTTGTTCTTTCTTTGGG 99
QY 344 GCACCTCTGACCTACTCTCCCGACATGAAGCGCTGAGCCGCGCTGCTGACGAG 403

Db 100 GACCTCTGACCTACCTCCCAAGATGAAAGGAGCTGAGCCGAGTGGCTGCTACAG 159
Qy 404 GGGGTGTGCTGCTGCTCGAAAGCACTGCGCATCGCCCGGAGCCGAGGAAAGGCGG 463
Db 160 GGGGTGTGCTGCTGCTCGAAAGCACTGCGCATCGCCCGGAGCCGAGGAAAGGCGG 219
Qy 464 GCAAGCTGAGAGCGCTGAGCTGCTGAGCAAGTAAACCACTCTACTCTCCGCTGCGG 523
Db 220 GCAAGCTGAGAGCGCTGAGCTGCTGAGCAAGTAAACCACTCTACTCTCCGCTGCGG 279
Qy 524 GAACTGTGATCCCGAGTCTCCGAGAGGCACTCAGCTTACCCAGTGAATCTTACAGCG 583
Db 280 GAACTGTGATCCCGAGTCTCCGAGAGGCACTCAGCTTACCCAGTGAATCTTACAGCG 339
Qy 584 GTCAATGACCTACCTTCTGAGCTGCTGAGTATCTCTGCGGAGCAAGCCCTGAGCCCT 643
Db 340 GTCAATGACCTACCTTCTGAGCTGCTGAGTATCTCTGCGGAGCAAGCCCTGAGCCCT 399
Qy 644 GATGAGCCCTCACTTCCATCCAGACAGCCGAGCTGCTCGGAACTGTCTATCTCCAG 703
Db 400 GATGAGCCCTCACTTCCATCCAGACAGCCGAGCTGCTCGGAACTGTCTATCTCCAG 459
Qy 704 GACAAAGAGAGCTTTTGGCACTGCTGCGCTGTCTGACACCTCCAGAACGAGGCTG 763
Db 460 GACAAAGAGAGCTTTTGGCACTGCTGCGCTGTCTGACACCTCCAGAACGAGGCTG 519
Qy 764 TGGGCGCCGCTTCTGCTGAGAGCCCGGAGACCTCTGCGGAGAACCCGAGAGGAG 823
Db 520 TGGGCGCCGCTTCTGCTGAGAGCCCGGAGACCTCTGCGGAGAACCCGAGAGGAG 579
Qy 824 TGGGCGCCCACTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 883
Db 580 TGGGCGCCCACTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 639
Qy 884 TGGGCTCAG 943
Db 640 TGGGCTCAG 699
Qy 944 CACCACTGAG 1003
Db 700 CACCACTGAG 758
Qy 1004 AGGCTGAG 1063
Db 759 AGGCTGAG 818
Qy 1064 GGTCTTCTGCTCTCTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1122
Db 819 GGTCTTCTGCTCTCTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 878
Qy 1123 GATATAG 1182
Db 879 GATATAG 937
Qy 1183 ATTAACTTTTATTAAAGTT 1203
Db 938 ATTAACTTTTATTAAAGTT 958

RESULT 2
US-08-466-127-1
Sequence 1, Application us/08466127
Patent No. 5683878

GENERAL INFORMATION:
APPLICANT: Elimeier, Willfried
APPLICANT: Weith, Andreas
TITLE OF INVENTION: Neuroblastoma-Associated Regulator Gene
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kesseler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, Suite 600
CITY: Washington

STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,127
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ramond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 0652,1360002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 982 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 37..481
US-08-466-127-1

Query Match 71.2%; Score 856.2; DB 1; Length 982;
Best Local Similarity 97.7%; Pred. No. 5,7e-231;
Matches 900; Conservative 0; Mismatches 18; Indels 3; Gaps 3;

Qy 284 GAGGCTGAG 343
Db 40 GATCTGACACAG 99
Qy 344 GCACTCTGAGTCACTCCCAAGATGAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 403
Db 100 GCACTCTGAGTCACTCCCAAGATGAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 159
Qy 404 GCGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 463
Db 160 GCGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 219
Qy 464 GCAAGCTGAG 523
Db 220 GCAAGCTGAG 279
Qy 524 GAACTGTGATCCCGAGTCTCCGAGAGGCACTCAGCTTACCCAGTGAATCTTACAGCG 583
Db 280 GAACTGTGATCCCGAGTCTCCGAGAGGCACTCAGCTTACCCAGTGAATCTTACAGCG 339
Qy 584 GTCAATGACCTACCTTCTGAGCTGCTGAGTATCTCTGCGGAGCAAGCCCTGAGCCCT 643
Db 340 GTCAATGACCTACCTTCTGAGCTGCTGAGTATCTCTGCGGAGCAAGCCCTGAGCCCT 399
Qy 644 GATGAGCCCTCACTTCCATCCAGACAGCCGAGCTGCTCGGAACTGTCTATCTCCAG 703
Db 400 GATGAGCCCTCACTTCCATCCAGACAGCCGAGCTGCTCGGAACTGTCTATCTCCAG 459
Qy 704 GACAAAGAGAGCTTTTGGCACTGCTGCGCTGTCTGACACCTCCAGAACGAGGCTG 763
Db 460 GACAAAGAGAGCTTTTGGCACTGCTGCGCTGTCTGACACCTCCAGAACGAGGCTG 519
Qy 764 TGGGCGCCGCTTCTGCTGAGAGCCCGGAGACCTCTGCGGAGAACCCGAGAGGAG 823
Db 520 TGGGCGCCGCTTCTGCTGAGAGCCCGGAGACCTCTGCGGAGAACCCGAGAGGAG 579
Qy 824 TGGGCGCCCACTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 883

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Db      580 TGGGCCCAACTTCGCCCTGCCACTTGACTTCACCAAAATCCCTTCCTGAGACTGAACC 639
Qy      884 TGGTCTCAGAGCGAAGGACTGTGAATCTTTAGCTGGAAGCCAGAGCTAGCTTGGC 943
Db      640 TGGTCTCAGAGCGAAGGACTGTGAATCTTTAGCTGGAAGCCAGAGCTAGCTTGGC 699
Qy      944 CACCAAGTGGGAGAGTCACTGCTGCCACCCCAAGTTCTAGAGCTTTTCAAG 1003
Db      700 CACCAAGTGGGAGAGTCACTGCTGCCACCCCAAGTTCTAGAGCTTTTCAAG 758
Qy      1004 AGCGTGAAGTGTGAAGAGAGTGTCTCTCCAACTATGCGCAAGCGCGGAGAGCT 1063
Db      759 AGCGTGAAGTGTGAAGAGAGTGTCTCTCCAACTATGCGCAAGCGCGGAGAGCT 818
Qy      1064 GGTCTTCTGCTCTCTCTGGAAGAAAGTGTGTGGCCCTGATTAAGTCTATATAG- 1122
Db      819 GGTCTTCTGCTCTCTCTGGAAGAAAGTGTGTGGCCCTGATTAAGTCTATATAG 878
Qy      1123 GTATATAGTGTGTGTATCACTTTTTCAGGGAGAGTGAATTTCTGTAACTGAGTGTAT 1182
Db      879 GTATATAGTGTGTGTATCACTTTTTCAGGGAGAGTGAATTTCTGTAACTGAGTGTAT 937
Qy      1183 ATTAACCTTTTATATAAGTT 1203
Db      938 ATTAACCTTTTATATAAGTT 958

RESULT 3
US-09-919-039-214
/ Sequence 214, Application US/09919039
/ Patent No. 6727066
/ GENERAL INFORMATION:
/ APPLICANT: Kaser, Matthew R.
/ TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
/ FILE REFERENCE: PA-0035 US
/ CURRENT APPLICATION NUMBER: US/09/919,039
/ PRIOR FILING DATE: 2002-09-09
/ PRIOR APPLICATION NUMBER: 60/222,113
/ NUMBER OF SEQ ID NOS: 401
/ SOFTWARE: PERL Program
/ SEQ ID NO 214
/ LENGTH: 653
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc feature
/ OTHER INFORMATION: Incyte ID No. 6727066 253987.16
US-09-919-039-214

Query Match      36.4%; Score 437.8; DB 4; Length 653;
Best Local Similarity 97.2%; Pred. No. 2.4e-113;
Matches 456; Conservative 0; Mismatches 12; Indels 1; Gaps 1;
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Qy      1036 CAAACTATGCCAAGGCGGCGGAGAGCTGTCTTCTGAGCTTGGAGAAAGTTCTGT 1095
Db      447 CAAACTATGCCAAGGCGGCGGAGAGCTGTCTTCTGAGCTTGGAGAAAGTTCTGT 506
Qy      1096 TGCCTGATTTATGAACCTATATATAG-GTATATAGTTTGTACTTTTTCACAGGAA 1154
Db      507 TGCCTGATTTATGAACCTATATATAGATATATAGTTTGTACTTTTTCACAGGA 566
Qy      1155 GGTGACTTCTGTAACTATGAGTATATTTAACTTTTATATAAGTT 1203
Db      567 GGTGACTTCTGTAACTATGAGTATATTTAACTTTTATATAAGTT 615

RESULT 4
US-08-256-077-3
/ Sequence 3, Application US/08256077
/ Patent No. 5654188
/ GENERAL INFORMATION:
/ APPLICANT: Blumel, Wilfried
/ APPLICANT: Welch, Andreas
/ TITLE OF INVENTION: Neuroblastoma-Associated Regulator Gene
/ NUMBER OF SEQUENCES: 6
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Steine, Kessler, Goldstein & Fox
/ STREET: 1100 New York Avenue, Suite 600
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: U.S.A.
/ ZIP: 20005-3934
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/256,077
/ FILING DATE: 23-JUNE-1994
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Esmond, Robert W.
/ REGISTRATION NUMBER: 32,893
/ REFERENCE/DOCKET NUMBER: 0652.1360000
/ TELEPHONE: (202) 371-2600
/ TELEFAX: (202) 371-2540
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 360 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
US-08-256-077-3

Query Match      29.9%; Score 360; DB 1; Length 360;
Best Local Similarity 100.0%; Pred. No. 1.4e-91;
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 181 GGCACCTACGCTTAGCCAGGTGGAATCTTACAGCGCGTCATCGACTACATTCTGACCTG 240
QY 608 CAGTAGTCTGCGGAGCCAGCCCTTGAAGGCCCCACCTTCCGATCCAG 667
DB 241 CAGTAGTCTGCGGAGCCAGCCCTTGAAGGCCCCACCTTCCGATCCAG 300
QY 668 ACAGCGAGCTGCTCCGGAATTGTCTCACTCAACGACAAAGAGCTTTTGCACCTGA 727
DB 301 ACAGCGAGCTGCTCCGGAATTGTCTCACTCAACGACAAAGAGCTTTTGCACCTGA 360

RESULT 5

US-08-466-127-3
Sequence 3, Application US/08466127
Patent No. 5683878
GENERAL INFORMATION:
APPLICANT: Elimeier, Wilfried
APPLICANT: Weich, Andreas
TITLE OF INVENTION: Neuroblastoma-Associated Regulator Gene
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,127
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Edmund, Robert W.
REGISTRATION/DOCKET NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 0652.1360002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2540
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..357
US-08-466-127-3

Query Match 29.9%; Score 360; DB 1; Length 360;
Best Local Similarity 100.0%; Pred. No. 1.4e-91;
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 368 ATGAAGGCGCTGAGCCCGGTGCGGCTGCTACGAGCGGTGCTGCTGCTGCGAAAGC 427
DB 1 ATGAAGGCGCTGAGCCCGGTGCGGCTGCTACGAGCGGTGCTGCTGCTGCGAAAGC 60
QY 428 AGCTGCGCATGCGCCGCGCGAGGGAAGGCGCGAGCTGAGAGCGCGCTGAAAGTTG 487
DB 61 AGCTGCGCATGCGCCGCGCGAGGGAAGGCGCGAGCTGAGAGCGCGCTGAAAGTTG 120
QY 488 CTGAGCAGCATGAGCACTGCTACTCCGCGCTGCGGGAATGTATACCGGAGTCCGAGA 547
DB 121 CTGAGCAGCATGAGCACTGCTACTCCGCGCTGCGGGAATGTATACCGGAGTCCGAGA 180
QY 548 GGCACCTACGCTTAGCCAGGTGGAATCTTACAGCGCGTCATCGACTACATTCTGACCTG 607

DB 181 GGCACCTACGCTTAGCCAGGTGGAATCTTACAGCGCGTCATCGACTACATTCTGACCTG 240
QY 608 CAGTAGTCTGCGGAGCCAGCCCTTGAAGGCCCCACCTTCCGATCCAG 667
DB 241 CAGTAGTCTGCGGAGCCAGCCCTTGAAGGCCCCACCTTCCGATCCAG 300
QY 668 ACAGCGAGCTGCTCCGGAATTGTCTCACTCAACGACAAAGAGCTTTTGCACCTGA 727
DB 301 ACAGCGAGCTGCTCCGGAATTGTCTCACTCAACGACAAAGAGCTTTTGCACCTGA 360

RESULT 6

US-08-256-077-5
Sequence 5, Application US/08256077
Patent No. 5654188
GENERAL INFORMATION:
APPLICANT: Elimeier, Wilfried
APPLICANT: Weich, Andreas
TITLE OF INVENTION: Neuroblastoma-Associated Regulator Gene
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,077
FILING DATE: 23-JUNE-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Edmund, Robert W.
REGISTRATION/DOCKET NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 0652.1360000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2540
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 446 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-256-077-5

Query Match 25.5%; Score 306.4; DB 1; Length 446;
Best Local Similarity 94.4%; Pred. No. 1.8e-76;
Matches 351; Conservative 0; Mismatches 16; Indels 5; Gaps 3;

QY 1 GATCTGCGGTGCTGCGCAGGAAAGCAAAATCTGGAAGTTAATGTTGAGTATCTT 60
DB 78 GATCTGCGGTGCTGCGCAGGAAAGCAAAATCTGGAAGTTAATGTTGAGTATCTT 137
QY 61 AATCTTGTCTGCGGAGAGCGCCGCTCTCCCGGATACAGCCCTTCTCATTTTGA 120
DB 138 AATCTTGTCTGCGGAGAGAGCAACCTCTCTCCCGGATACAGCCCTTCTCATTTTGT 197
QY 121 ATCCGCGGCTCGCGGCTTCTGCGGTACAGACACCGGAGAGAGCTGTTTGCATTAA 180
DB 198 ATCCGCGGCTCGCGGCTTCTGCGGTACAGACACCGGAGAGAGCTGTTTGCATTAA 257
QY 181 GCGGCTGTGAAGCCCAAGGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 239
DB 258 GCGGCTGTGAAGCCCAAGGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 317
QY 240 AGAGCGTGCCTTCCAGGAGGCTCTTAAGTAGACCGCGCGGCGGCGGCGGCGGCGGCTTG 299

D _b	318	AGAGCGCTGCTTCACGACAGGCTCATAGAGACCGCGCGG---	CGACGTGCGCCGTG	374
Q _y	300	CAGGTCACTGTAGC-GGACTCTTTTGGTTTTCTTCTCTTTGGGCACTCTGGACTCA		358
D _b	375	CAGGTCACTGTAGCGGACTCTTTTGGTTTTCTTCTTTGGGGCACTCTGGACTCA		434
Q _y	359	CTCCCCGACATG	370	
D _b	435	CTCCCCGACATG	446	

RESULT 7

US-08-466-127-5
 Sequence 5, Application US/08466127
 Patent No. 5683878
 GENERAL INFORMATION:
 APPLICANT: Elmeier, Wilfried
 APPLICANT: Welch, Andreas
 TITLE OF INVENTION: Neuroblastoma-Associated Regulator Gene
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
 STREET: 1100 New York Avenue, Suite 600
 CITY: Washington
 STATE: D.C.
 COUNTRY: U.S.A.
 ZIP: 20005-3934
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/466,127
 FILING DATE: 06-JUN-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Esmond, Robert W.
 REGISTRATION NUMBER: 32,893
 REFERENCE/DOCKET NUMBER: 0652.1360002
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 371-2600
 TELEFAX: (202) 371-2540
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 446 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-466-127-5

	Query Match	Similarity	Score	306.4	DB 1	Length	446			
	Best Local	Similarity	94.4%	Pred.	No.1.8e-76					
	Matches	351	Conservative	0	Mismatches	16	Indels	5	Gaps	3
QY	1	GATCTGGGGTGTCTGCACGAAAAAGCAAAATTCGTGAAGTTAA	TGTTTTGAGTGATCTT	60						
DB	78	GATCTGGGGTGTCTGCACGAAAAAGCAAAATTCGTGAAGTTAA	TGTTTTGAGTGATCTT	137						
QY	61	AAATCTTGTCTGGCGGAGAGGCGCGCTTCCCGGATCAGCGCTTCTCATTTCTTGA	120							
DB	138	AAATCTTGTCTGGCGGAGAGAGCCACTTCTCCCGGATCAGCACTTCTCATTTCTTAT	197							
QY	121	ATCCGCGGCTCCGCGGTCCTTGGCGCTCAACACGACGCGAGAGAAGCTGTTTGCAATTTAA	180							
DB	198	ATCCAGGCTCCGCGGTCCTTGGCGCTCAACACGACGCGAGAGAAGCTGTTTGCAATTTAA	257							
QY	181	GCGGCGCTGTGAACGCCCAAGGCGCGGCGGGGCGGGGCCGA-GCGGGGCCATTTTGAATTA	239							
DB	258	GCGGCGCTGTGTACCCCAAGGGCCGACGCGGGCGGGGCCGAGGGCGGGCCATTTTGAATTA	317							

QY	240	AGAGGGGTGCTCTTCAAGGAGGCTTATTAAGGACCGCGGAGCGTGGCGCTTG	299
Db	318	AGAGGGGTGCTCTTCAAGGAGGCTTATTAAGGACCGCGGCGG---GCACGTGGCGCTG	374
QY	300	CAGGTACCTGPAAGC-GGACTCTTTGGTTTTCTTCTCTTGGGGGACCTGTGACTCA	358
Db	375	CAGGTACCTGTAAGCGGACTCTTTGGTTTTCTTCTCTTTGGGGACCTGTGACTCA	433
QY	359	CTCCCGACGATG	370
Db	435	CTCCCGACGATG	446

RESULT 8

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US-09-513-999C-23008
; Sequence 23008, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclet, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins
; Patent No. 6783961
; FILE REFERENCE: 59 US2, RG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 23008
; LENGTH: 255
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 42
; OTHER INFORMATION: w=a or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 108
; OTHER INFORMATION: w=a or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 220
; OTHER INFORMATION: n=a, g, c or t
US-09-513-999C-23008

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Query Match	16.5%	Score 198.4;	DB 4;	Length 255;
Best Local Similarity	99.0%	Pred. No. 3.5e-46;		
Matches 199; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0

Qy	1	AATCGGGGAGCTCGCAGAGAAAACCAAAATCTGGAAGTTATGGTTTGAAGGATCTT	60
Db	51	GATCTGGGGGTCTCGCAGAGAAAACCAAAATCTGGAAGTTATGGTTTGAAGGATTTT	110
Qy	61	AAATCTTGTCTGGCGAGAGGCGCCGCTCTCCCGGTATCAGCGCTTCTCATTTCTTGA	120
Db	111	AAATCTTGTCTGGCGAGAGGCGCCGCTCTCCCGGTATCAGCGCTTCTCATTTCTTGA	170
Qy	121	ATCGCGGCTCCGCGGCTCTTGGGCTCAGACCAAGCGAGAGAACTGTTTGCATTTAA	180
Db	171	ATCGCGGCTCCGCGGCTCTTGGGCTCAGACCAAGCGAGAGAACTGTTTGCATTTAA	230
Qy	181	GGCGGCTTGAAACGCCCAAGG	201
Db	231	GGCGGCTTGAAACGCCCAAGG	251

RESULT 9

US-08-151-391A-3
; Sequence 3, Application US/08151391A
; Patent No. 5527897

```

1 GENERAL INFORMATION:
2 APPLICANT: Oda, Kinichiro
3 APPLICANT: Nakada, Susumu
4 APPLICANT: Hara, Ei-ji
5 APPLICANT: Yamaguchi, Tomoko
6 APPLICANT: Nakamura, Takeshi
7 APPLICANT: Oka, Yumiko
8 APPLICANT: Kishimoto, Toshiko
9 TITLE OF INVENTION: Human ID Genes
10 NUMBER OF SEQUENCES: 8
11 CORRESPONDENCE ADDRESS:
12 ADDRESSEE: LOWE, PRICE, LEBLANC & BECKER
13 STREET: 99 Canal Center Plaza, Suite 300
14 CITY: Alexandria
15 STATE: Virginia
16 COUNTRY: U.S.A.
17 ZIP: 22314
18 COMPUTER READABLE FORM:
19 MEDIUM TYPE: Floppy disk
20 COMPUTER: IBM PC compatible
21 OPERATING SYSTEM: PC-DOS/MS-DOS
22 SOFTWARE: Patent.in Release #1.0, Version #1.25
23 CURRENT APPLICATION DATA:
24 APPLICATION NUMBER: US/08/151,391A
25 FILING DATE: 12-NOV-1993
26 CLASSIFICATION: 536
27 ATTORNEY/AGENT INFORMATION:
28 NAME: Mills, Demetra J.
29 REGISTRATION NUMBER: 34,506
30 REFERENCE/DOCKET NUMBER: 715-087
31 TELECOMMUNICATION INFORMATION:
32 TELEPHONE: (703)684-1111
33 TELEFAX: (703)684-1124
34 TELEX: 82-4425
35 INFORMATION FOR SEQ ID NO: 3:
36 SEQUENCE CHARACTERISTICS:
37 LENGTH: 502 base pairs
38 TYPE: nucleic acid
39 STRANDEDNESS: double
40 TOPOLOGY: linear
41 MOLECULE TYPE: cDNA to mRNA
42 HYPOTHETICAL: NO
43 ANTI-SENSE: NO
44 FEATURE:
45 NAME/KEY: misc.feature
46 LOCATION: 22..765
47 OTHER INFORMATION: /note="CDS"
48 JS-08-151-391A-3

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	Query Match	6.2%;	Score 75;	DB 1;	Length 502;
	Best Local Similarity	58.0%;	Pred. No. 2.4e-11;		
	Matches 163;	Conservative	0;	Mismatches 100;	Indels 18; Gaps 1
Qy	369	TGAAGCGCGTGAGCCCGGCGTGC	CGCGCTCTCAAGAGCGCGTGTGCTGCTGCTCGGAACGA	428	
Db	77	TGAAGCGCGGCAAGACAGCAGCGGTGGGGCGAGGTGTGCTGTCTGTCTTGAGCAGA	136		
Qy	429	GTCTGGCCATCGCCCGGGGCCGAGGAAAGGCCCGGCACTGAGAGACCGCTGAGCT	485		
Db	137	GCCTGGCCATCTCGCGCTGCGGGGCGCGGGGGCGCGCTGCTGCTGTGTGAGCAGC	196		
Qy	486	-----TGCTGACGACATGAAACATCTGACTCCCGCGCTGCGGAACTG	530		
Db	197	AGCAGGTAAACGTGCTGCTCTCAACGACATGAACCGGTCTTACTACACGCTCAAGAGGCTGG	256		
Qy	531	TACCCGGAATCCCGAGAGGCACTCAGCTTAAGCCAGGTGAAATCTTACAGCGGTCAATG	550		
Db	257	TGCGCACCGTGGCCCCAGAAACCGCAAGGTGAGAGAGGTGAATTTCTCCAGCAGTATCG	316		
Qy	591	ACTACATTTCCAGCCGAGGAGTGTCTGCGCGAGCCAGCC	631		
Db	317	ACTACATCAAGGACCTTCAGTTGAGGCTGAATCTCGAAATCC	357		

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RESULT 10
US-09-561-497-3
; Sequence 3, Application US/09561497
; Patent No. 637243
; GENERAL INFORMATION:
; APPLICANT: Brenda F. Baker
; APPLICANT: C. Frank Bennett
; TITLE OF INVENTION: JACQUELINE WYATT
; FILE REFERENCE: RTS-0149
; CURRENT APPLICATION NUMBER: US/09/561,497
; CURRENT FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 3
; LENGTH: 926
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (36)... (500)
US-09-561-497-3

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Query Match	6.2%	Score 75	DB 3	Length 926	
Best Local Similarity	58.0%	Pred. No. 3.1e-11			
Matches 163	Conservative	0	Mismatches 100	Indels 18	Gaps 1
Qy	369	TGAAGGCGCTGAGCCCGGTGCGCGGCTTCTACAGAGCGGTGTGCTGCCTGTGCAACGA	428		
Db	91	TGAAGCGCGGCAAGACAGCGAGCGGTGGGGCGAGGTGTGTCTGTCTGACGAGA	150		
Qy	429	GTCGTGCCATGCCCGGGGCGGAGGGAAGGCGCGGACGTGAGAGCGCGTGAAGCT---	485		
Db	151	GCGTGGCCATCTCGGCGTGGCGGGGCGCGGGGCGCGCGTGCCTGCTGACGAGC	210		
Qy	486	-----TGCTGACGACATGAACCACTGCTACTCCCGCTGCGGGAATCG	530		
Db	211	AGCAGGTAAACGTGTGCTTACGACATGAACCGGTGTTACTCAACGCTCAAGAGACTGG	270		
Qy	531	TACCGGAGTCCCGAGAGGCACTACGTTACCGAGTGAATCTCAAGGCGGCAATCG	590		
Db	271	TGCCACCCCTGCCCGAAGCCGCAAGGTGACGAAAGTGAATTTCCAGACGTCATCG	330		
Qy	591	ACTACATTCTGCACCTGCAGGTAGTCTGGCGGACCGC	631		
Db	331	ACTACATCAGGACCTTCAATTGAGACTGAACCTCGAAATCC	371		

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RESULT 11
/ Sequence 1, Application US/08151391A
/ US-08-151-391A-1
/ Patent No. 5527897
/ GENERAL INFORMATION:
/ APPLICANT: Oda, Kinichiro
/ APPLICANT: Nakada, Susumu
/ APPLICANT: Hara, Eiji
/ APPLICANT: Yamaguchi, Tomoko
/ APPLICANT: Nakamura, Takeshi
/ APPLICANT: Oka, Yumiko
/ APPLICANT: Kishimoto, Toshiniko
/ TITLE OF INVENTION: Human ID Genes
/ NUMBER OF SEQUENCES: 8
/ CORRESPONDENCE ADDRESS:
/ ADDRESSSEE: LOWE, PRICE, LEBLANC & BECKER
/ STREET: 99 Canal Center Plaza, Suite 300
/ CITY: Alexandria
/ STATE: Virginia
/ COUNTRY: U.S.A.
/ ZIP: 22314
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS

```

SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/151,391A
FILING DATE: 12-NOV-1993
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: M118, Demetra J.
REGISTRATION NUMBER: 34,506
REFERENCE/DOCKET NUMBER: 715-087
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 684-1111
TELEFAX: (703) 684-1124
TELEX: 82-4425
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 509 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cdna to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: 22..483
OTHER INFORMATION: /note= "CDS"
US-08-151-391A-1

Query Match 5.1%; Score 73.4; DB 1; Length 509;
Best Local Similarity 57.7%; Pred. No. 6,8e-11;
Matches 162; Conservative 0; Mismatches 101; Indels 18; Gaps 1;

QY 359 TGAAGCGCTGAGCCCGGTCGCGCTGCTACGAGCGCGTGTGCTGCTGTGCGAAGCCA 428
DB 77 TGAAGCGCGGGAAGACAGAGCGGAGGCGGAGGCGGAGGCGGCTGTGCTGTGAGCA 136
QY 429 GTCTGGCCATCGCCCGGCGGCGGAGGAGGCGCCGCGACGCTGAGGACCGCTGAGCT--- 485
DB 137 GCGTGGCCATCTCGGCTGCGCGGCGGCGGCGCGCGCTGCTGCTGCTGAGCAAGC 196
QY 486 -----TGCAGACGACATGAAACACTGCTACCTCCGCGCGGGAACCTGG 530
DB 197 AGCAGTAAACGTGCTGCTTACGACATGAAACGCTGTACGACCTCAAGAGAGCTGG 256
QY 531 TACCGGAGTCCCGAGAGGCACTGAGCTTAGCGAGGTGGAATCTTACAGCGCGTCATCG 590
DB 257 TGCCCAACCTGCGCCAGAACCGCAAGGTGAGCTGAGATTTCTCCAGCAGTCATCG 316
QY 591 ACTACATTCTGACCTGACGAGGTAGTCTGGCCGAGCCAGCC 631
DB 317 ACTACATCAGGAGCCTTGTGAGCTGAACTCGAATTC 357

RESULT 12
US-09-561-497-10
Sequence 10, Application US/09561497
Patent No. 637243
GENERAL INFORMATION:
APPLICANT: Brenda F. Baker
APPLICANT: C. Frank Bennett
APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION: ANTISENSE MODULATION OF INHIBITOR OF DNA BINDING-1 EXPRESSION
FILE REFERENCE: RFS-0149
CURRENT APPLICATION NUMBER: US/09/561,497
CURRENT FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 88
SEQ ID NO 10
LENGTH: 4793
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:

NAME/KEY: CDS
LOCATION: (2210) ... (2659)
US-09-561-497-10

Query Match 5.8%; Score 70; DB 3; Length 4793;
Best Local Similarity 59.2%; Pred. No. 1.6e-09;
Matches 168; Conservative 0; Mismatches 95; Indels 21; Gaps 2;

QY 359 TGAAGCGCTAGCCCGGTGGCGGCTCTCTACGAGCGGTGTGCTGCTGTGCGAAGCCA 428
DB 2265 TGAAGCGCGGGAAGACAGCGAGCGGTGCGGCGAGGTGTGCTGCTGTGAGCA 2324
QY 429 GTCTGGCCATCGCCCGGCGGCGGAGGAGGCGCGGCA-----GCTG 470
DB 2325 GCGTGGCCATCTCGGCTGCGCGCGGCGGCGCGCGCTGCTGCTGCTGAGC 2384
QY 471 AGAGCGCGCTGAGCTTGTG---GACATAGAACCACTGTACTCCGCGCTGCGGGAAC 527
DB 2385 AGCAGAGGTAAAGCTGTGCTGTACGACATGAAAGCGCTTACTACGCGCTCAAGAGC 2444
QY 528 TGTACCGGAGTCCCGAGAGCACTACGCTTAGCGAGGTGGAATCTTACAGCGCGTCA 587
DB 2445 TGTGCCCCACCTGCGCCGAGAACCGCAAGGTGAGCAAGTGTGAGATTCCTCCAGCAGTCA 2504
QY 588 TCGACTACATCTGACCTGAGGAGTGTCTGGCCGAGCCAGCC 631
DB 2505 TCGACTACATCAGGAGCCTTCACTTGTGAGCTGAACTCGAATTC 2548

RESULT 13
US-08-896-164-30
Sequence 30, Application US/08896164
Patent No. 6218521
GENERAL INFORMATION:
APPLICANT: OBATA, Yutachi
TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES ASSOCIATED
TITLE OF INVENTION: WITH GASTRIC CANCER AND METHODS FOR
TITLE OF INVENTION: DIAGNOSING AND TREATING GASTRIC CANCER
NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44mb
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/896,164
FILING DATE: July 17, 1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: No. 6218521man D. Hanson
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5499 - JEL/NDH/SLH
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 721 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-896-164-30
Query Match 5.7%; Score 69; DB 3; Length 721;
Best Local Similarity 58.8%; Pred. No. 1.4e-09;
Matches 167; Conservative 0; Mismatches 96; Indels 21; Gaps 2;

QY 369 GGAAGCGCGTGAAGCCCGGTGCGCGGTGCTGAAGAAGCGGTGTCTGCTGTGCGAAACGA 428

Db 118 TGAAGCGCGCGCAAGAGCGAGCGGGCGGGCGAGGTGTGTGTGCGCTGTCTGTGACACGA 1777

QY 429 GTCTGGCCATCGCGCGGGGCGAGGGAGAGGCCCGCA-----GCTG 470

Db 178 GGTGGCCATCTCGGCTGTGCGGGGGGCGGGGCGGCGCTGTGCGCTGTGACG 237

QY 471 AGGAGCCCGTGAAGCTTGTCTG---GAGCATATGAACCATCTGTACTCTCCGCTGCGGGAAC 527

Db 238 AGCAGCAGGTAAACGTGCTGTCTTAAACATGAAACGGCTGTACTACCGCTTAAAGAGC 297

QY 528 TGGTATCCGGAATCCCGAAGGACACTCAGCTTAGCAGGATGAATCTTAACAGCGGTCA 587

Db 298 TGGTCCCAACCTGTGCCCCGAAGCCGCAAGGTAGCAAGATGAGATTTCTTCAGCACTCA 357

QY 588 TCGACTACATTTCCGACTGTGCAAGTAGTCTTGGCCGACCGACGC 631

Db 358 TCGACTACATCAGGAGCCTTTCAGTTGAGACTGAATCCGGAATCC 401

```

RESULT 14
US-09-621-976-2005
/ Sequence 2005, Application US/09621976
/ Patent No. 6639063
/ GENERAL INFORMATION:
/ APPLICANT: Dumas Milne Edwards, J.B.
/ APPLICANT: Jobert, S.
/ APPLICANT: Giordano, J.Y.
/ TITLE OF INVENTION: ESTs and Encoded Human Proteins
/ FILE REFERENCE: GENSET .054PR2
/ CURRENT APPLICATION NUMBER: US/09/621,976
/ CURRENT FILING DATE: 2000-07-21
/ NUMBER OF SEQ ID NOS: 19335
/ SOFTWARE: Patent.jp
/ SEQ ID NO 2005
/
/ LENGTH: 626
/
/ TYPE: DNA
/
/ ORGANISM: Homo sapiens
/
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 211..570
/ NAME/KEY: sig_peptide
/ LOCATION: 211..378
/ OTHER INFORMATION: Von Heijne matrix
/ OTHER INFORMATION: score 3.55999990463257
/ OTHER INFORMATION: seq LOGITGLAXPLX/DL
US-09-621-976-2005

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Query Match	5.2%	Score 62.8	DB 4	Length 626
Best Local Similarity	55.1%	Pred. No. 7.1e-08		
Matches 173	Conservative 7	Mismatches 125	Indels 9	Gaps 3
OY	412 CTGCTTGTGGAAAGCAGTCTTGSGCCATTCGCGCGGGCCGAGGGAAAGGCGCCGGCAGCTGA	471		
Db	152 CAGCTCTGTGCGACCAAGCGCTGGGATCTTAAACGGAGCAAAACCCCTGTGACAGACCCGA	211		
OY	472 GGAGCGCGTGAAGCTTGCTGGACGACATGAACCACTGCTCTCCCGCTCTGCGGGAACTGGT	531		
Db	212 TGAGC-----CTGKSTATTACAAATGAACGACATGCTCTACTCCAAAGCTCAAGAGCTTGGT	264		
OY	532 ACCCGGAAGTCCCGAAGAGGCATCTCAGCTTAAAGCCAGGTGAAGAAATCTTACAGCGCGT-CATCG	590		
Db	265 GCCCGCAGCATCCCCCGAGAACAGAAAGGTGAGCAAGATGGAATACTCTGCACACGTCATATG	324		
OY	591 ACTACAT-TCTTGACCTTGAGGAGTGGCTCGGGCGAGCCAGCCCGCTGACACCCCTGATATGGC	649		
Db	325 ACTAATCTTGGGAACTCGAGATTCGCCCTTGGGAACTCGCATTHCCCACTATTGTSAGACCTTG	384		
OY	650 CCCCACTTTCCATTCAGACAGCCCGAGCTCGCTCCGGAACTTGTCATCTTCCACAGCAAA	709		
Db	385 CATCAACCCAGAGACCCGGGGGAGAAACAGGCGCTTCAGAGACGGGGCTTGGACACACCTCCAC	444		

Qy 710 AGAGCTTTGCCA 723
| | | | |
Db 445 ACGGATATCAGCA 458

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1      RESULT 15
2      US-08-362-495-4
3      : Sequence 4, Application US/08362495
4      : Patent No. 6087171
5      :
6      : GENERAL INFORMATION:
7      : APPLICANT: Neuman, Toomas
8      : APPLICANT: Sude, Kikuo
9      : APPLICANT: No. 608717nes, Howard O.
10     : TITLE OF INVENTION: METHOD FOR INDUCING DNA SYNTHESIS IN
11     : TITLE OF INVENTION: NEURONS
12     : NUMBER OF SEQUENCES: 5
13     : CORRESPONDENCE ADDRESS:
14     : ADDRESSEE: Fanning, Henderson, Farabow, Garrett &
15     : ADDRESSEE: Dunne, L.L.P.
16     : STREET: 1300 I Street, N.W.
17     : CITY: Washington
18     : STATE: D.C.
19     : COUNTRY: U.S.A.
20     : ZIP: 20005-3315
21     :
22     : COMPUTER READABLE FORM:
23     : MEDIUM TYPE: Floppy disk
24     : COMPUTER: IBM PC compatible
25     : OPERATING SYSTEM: PC-DOS/MS-DOS
26     : SOFTWARE: PatentIn Release #1.0, Version #1.30
27     : CURRENT APPLICATION DATA:
28     : APPLICATION NUMBER: US/08/362,495
29     : FILING DATE: 18-NOV-1996
30     : CLASSIFICATION: 435
31     :
32     : PRIOR APPLICATION DATA:
33     : APPLICATION NUMBER: WO PCT/US94/14614
34     : FILING DATE: 19-DEC-1994
35     :
36     : PRIOR APPLICATION DATA:
37     : APPLICATION NUMBER: US 08/301,416
38     : FILING DATE: 08-SEP-1994
39     :
40     : PRIOR APPLICATION DATA:
41     : APPLICATION NUMBER: US 08/169,522
42     : FILING DATE: 15-DEC-1993
43     :
44     : ATTORNEY/AGENT INFORMATION:
45     : NAME: Barker, M. Paul
46     : REGISTRATION NUMBER: 32,013
47     : REFERENCE/DOCKET NUMBER: 05800.0001-02000
48     : TELECOMMUNICATION INFORMATION:
49     : TELEPHONE: 202-408-4000
50     : TELEFAX: 202-408-4400
51     :
52     : INFORMATION FOR SEQ ID NO: 4:
53     : SEQUENCE CHARACTERISTICS:
54     : LENGTH: 1309 base pairs
55     : TYPE: nucleic acid
56     : STRANDEDNESS: single
57     : TOPOLOGY: linear
58     :
59     : MOLECULE TYPE: DNA (genomic)
60     :
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Query Match	4.0%;	Score 47.6;	DB 3;	Length 1309;
Best Local Similarity	57.0%;	Pred. No. 0.0018;		
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QY	456	AGGACCCGGCAGCTGAGAGACCCGCTGAGCTTGTTCGACGACATGAAACCACTGCTACTCC	515	
Db	388	AGGGGGGGCGCGAATGAGACCGGGCGCTGTGCTTCGAGTGGATGAAACGACCTGCTACAGTC	447	
QY	516	GCCCTGCGGAACTTGTAACCCGAGTCCCGAGAGGCACTCAGCTTATGCCAGGTGAAATCC	575	
Db	448	G-CTGGGAGGCTGTGCTTACATCCCGGCCCAAGAAAGTCAGCAAAAGTGAGATCC	506	
QY	576	TACAGCGCTTCATGACTACTATTCGACCTGACAGTAGTCTGAGCGAGGCCCTGTG	635	

Db	507	TGCAGCTGCGCTGGAGACTCACCCTGCTTTGCTGAGACAGCCGCCACCGCCGCCAC	566
Qy	636	GACCCC	641
Db	567	CTCTCC	572

Search completed: December 18, 2004, 20:46:24
Job time : 122.791 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 18, 2004, 15:09:16 ; Search time 706.883 Seconds
(without alignments)
9395.574 Million cell updates/sec

Title: US-09-996-529A-5

Perfect score: 1203

Sequence: 1 gatcgggggctgctgcagga.....ttaacttttataaagct 1203

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4093002 seqs, 276041825 residues

Total number of hits satisfying chosen parameters: 8186004

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1178.4	98.0	1203	US-10-171-581-258	Sequence 258, App
2	1178.4	98.0	1203	US-10-450-826-22	Sequence 22, App1
3	1164.2	96.8	2066	US-10-116-802-341	Sequence 341, App
4	1164.2	96.8	2066	US-10-084-817-263	Sequence 263, App
5	1162.8	96.7	1300	US-09-925-298-39	Sequence 39, App1
6	1162.8	96.7	1300	US-10-103-806-39	Sequence 39, App1
7	950.8	79.0	1504	US-10-198-846-13483	Sequence 13483, A
8	856.2	71.2	982	US-10-450-826-21	Sequence 21, App1
9	663.8	55.3	2481	US-10-450-826-23	Sequence 23, App1
c 10	652.8	54.3	129722	US-10-450-826-24	Sequence 24, App1
c 11	437.8	36.4	653	US-09-919-039-214	Sequence 214, App
c 12	437.8	36.4	2066	US-10-116-802-341	Sequence 341, App

c	13	437.8	36.4	2066	15	US-10-084-817-263	Sequence 263, App
	14	425	35.3	465	10	US-09-918-995-11450	Sequence 11450, A
	15	422.6	35.1	429	10	US-09-918-995-8760	Sequence 8760, App
	16	358.4	29.8	360	17	US-10-384-339C-88	Sequence 88, App1
	17	354	29.4	531	15	US-10-029-386-9621	Sequence 9621, App
	18	345.8	28.7	568	16	US-10-152-319A-1595	Sequence 1595, App
	19	335.4	27.9	517	18	US-10-363-345A-26391	Sequence 26391, A
	20	335.4	27.9	517	18	US-10-363-345A-26392	Sequence 26392, A
	21	309	25.7	495	9	US-09-864-761-19607	Sequence 19607, A
	22	296.2	24.6	517	18	US-10-363-345A-26389	Sequence 26389, A
	23	296.2	24.6	517	18	US-10-363-345A-26390	Sequence 26390, A
	24	285	23.7	285	15	US-10-029-386-23321	Sequence 23321, A
	25	258	21.4	258	9	US-09-796-692-9456	Sequence 9456, App
	26	258	21.4	258	14	US-10-040-662-9456	Sequence 9456, App
	27	258	21.4	258	16	US-10-057-475B-9456	Sequence 9456, App
	28	258	21.4	258	16	US-10-154-884B-9456	Sequence 9456, App
	29	258	21.4	258	17	US-10-764-324-9456	Sequence 9456, App
	30	246	20.4	528	16	US-10-388-934-658	Sequence 658, App
	31	189.6	15.8	247	16	US-10-242-535A-28198	Sequence 28198, A
	32	189.6	15.8	247	16	US-10-085-783A-28198	Sequence 28198, A
	33	171.6	14.3	926	14	US-10-198-846-6871	Sequence 6871, App
	34	144.4	12.0	215	16	US-10-242-535A-8033	Sequence 8033, App
	35	144.4	12.0	215	16	US-10-085-783A-8033	Sequence 8033, App
	c 36	125.8	10.5	337	17	US-10-469-285-573	Sequence 573, App
	c 37	121	10.1	133	9	US-09-815-343-13	Sequence 13, App1
	c 38	121	10.1	133	9	US-09-815-343-619	Sequence 619, App
	c 39	121	10.1	133	9	US-09-815-343-1374	Sequence 1374, App
	40	121	10.1	133	9	US-09-815-343-1432	Sequence 1432, App
	c 41	121	10.1	133	16	US-10-097-105-13	Sequence 13, App1
	c 42	121	10.1	133	16	US-10-097-105-619	Sequence 619, App1
	c 43	121	10.1	133	16	US-10-097-105-1374	Sequence 1374, App
	44	121	10.1	133	16	US-10-097-105-1432	Sequence 1432, App
	45	119.4	9.9	133	9	US-09-815-343-1000	Sequence 1000, App

ALIGNMENTS

RESULT 1
US-10-171-581-258
; Sequence 258, Application US/10171581
; Publication No. US20030104426A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: Linley, Peter
; TITLE OF INVENTION: Signature Genes in Chronic Myelogenous Leukemia
; FILE REFERENCE: 9301-157-999
; CURRENT APPLICATION NUMBER: US/10/171,581
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/298,914
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 366
; SEQ ID NO 258
; LENGTH: 1203
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: X69111
; DATABASE ENTRY DATE: 2001-06-18
US-10-171-581-258

Query Match 98.0%; Score 1178.4; DB 15; Length 1203;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1201; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

Qy	1	GATCGGGGCTGCTGCAGAAAGCAATTCGAAATGATGCTTGTGAGTATCTT	60
Db	1	GATCGGGGCTGCTGCAGAAAGCAATTCGAAATGATGCTTGTGAGTATCTT	60
Qy	61	AAATCTTCTGCGGAGAGCCCGCTCTCCCGATACAGCGCTTCTCATTTTGA	120
Db	61	AAATCTTCTGCGGAGAGCCCGCTCTCCCGATACAGCGCTTCTCATTTTGA	120

OY	121	ATCCCGGGCTCGCGGCTCTTCGGCGTCAGACCAGCGGAGAGCGCTGTTGCAATTTAA	187
Db	121	ATCCCGGGCTCGCGGCTCTTCGGCGTCAGACCAGCGGAGAGCGCTGTTGCAATTTAA	187
OY	181	GGGGCTGTGAACGCCACGAGGGCCGGGGCGGGGCGGAGCGGGCCATTGTAATAA	240
Db	181	GGGGCTGTGAACGCCACGAGGGCCGGGGCGGGGCGGAGCGGGCCATTGTAATAA	240
OY	241	GAGGCTGCTTCCAGGCAAGGCTATTAAGTACCGCGCGGCAGAGTGCAGCGCTTGC	300
Db	241	GAGGCTGCTTCCAGGCAAGGCTATTAAGTACCGCGCGGCAGAGTGCAGCGCTTGC	300
OY	301	AGGTCACTGTAGCGGACTTTGGTTTTCTTCTCTTTGGGGACCTTCGACTCACT	360
Db	301	AGGTCACTGTAGCGGACTTTGGTTTTCTTCTCTTTGGGGACCTTCGACTCACT	360
OY	361	CCCCAGCATGAAAGCGCTGAGCCCGGATGCGCGCTGCTACGAGCGGTGCTGCCGTG	420
Db	361	CCCCAGCATGAAAGCGCGCTGAGCCCGGATGCGCGCTGCTACGAGCGGTGCTGCCGTG	420
OY	421	GGAAGCAGTCTGGCCANTGCGCCGGGGCCGAGGGAAGGCCCCGACGCTGAGAGCGCT	480
Db	421	GGAAGCAGTCTGGCCANTGCGCCGGGGCCGAGGGAAGGCCCCGACGCTGAGAGCGCT	480
OY	481	GAGCTTCTGACGACATGAAACACTGCTATCCTCCGCTGCGGGAACTGGTACCGGAGT	540
Db	481	GAGCTTCTGACGACATGAAACACTGCTATCCTCCGCTGCGGGAACTGGTACCGGAGT	540
OY	541	CCGAGAGGGAATCAGCTTACGCAAGGTGGAATTCCTACAGCGCTCATCGACTACATTCCT	600
Db	541	CCGAGAGGGAATCAGCTTACGCAAGGTGGAATTCCTACAGCGCTCATCGACTACATTCCT	600
OY	601	GACCTTGACAGTACTCTGCGCGAGCGACGCCCTGAGCCCGTGAATGGGCCCCACCTTCC	660
Db	601	GACCTTGACAGTACTCTGCGCGAGCGACGCCCTGAGCCCGTGAATGGGCCCCACCTTCC	660
OY	661	CATCCAGACAGCCGAGCTGCTCCGGAATTGTCATCTCCAAAGCAAAAGAGCTTTTG	720
Db	661	CATCCAGACAGCCGAGCTGCTCCGGAATTGTCATCTCCAAAGCAAAAGAGCTTTTG	720
OY	721	CCACTGACTCGGCGGTGCTGACACCTCCAGAACGAGAGTCTGGCGCCGTTCTGCT	780
Db	721	CCACTGACTCGGCGGTGCTGACACCTCCAGAACGAGAGTCTGGCGCCGTTCTGCT	780
OY	781	GGGACCCCGGGAACCTCTCTGCGCGGAAGCGGACGAGGATGGGCCCAACTTGC	840
Db	781	GGGACCCCGGGAACCTCTCTGCGCGGAAGCGGACGAGGATGGGCCCAACTTGC	840
OY	841	CTGCCACCTTGACTTCAACCAAAATCCCTCTCGGAGACTTAACCTGTGCTCAGAGCGAA	900
Db	841	CTGCCACCTTGACTTCAACCAAAATCCCTCTCGGAGACTTAACCTGTGCTCAGAGCGAA	900
OY	901	GGACTGTGAATTGTAGCTTGAAAGCGCAGAGCTGACTCTGGCCACAGCTGGGCGAGT	960
Db	901	GGACTGTGAATTGTAGCTTGAAAGCGCAGAGCTGACTCTGGCCACAGCTGGGCGAGT	960
OY	961	CACCTGTGCCACCCCAACCCCCAAAGTTCTAAAGCTTTTCAAGAGCGTGAAGGTGGA	1020
Db	961	CACCTGTGCCACCCCAACCCCCAAAGTTCTAAAGCTTTTCAAGAGCGTGAAGGTGGA	1020
OY	1021	GGAAGTGTGCTTCCCAAACTATGCGAGGCGGCGGCACTGAGTCTTCTGCTCTCT	1080
Db	1021	GGAAGTGTGCTTCCCAAACTATGCGAGGCGGCGGCACTGAGTCTTCTGCTCTCT	1080
OY	1081	GGAAGAGGTCTGTGGCTGATTTATGAATCTCATPATAG-GTATPATAGTTTGTAC	1139
Db	1081	GGAAGAGGTCTGTGGCTGATTTATGAATCTCATPATAGGTATPATAGTTTGTAC	1140
OY	1140	CTTTTTCAGAGGAAGTGACTTCTGTGAACAAGCATGATATTAACCTTTTATATA	1199
Db	1141	CTTTTTCAGAGGAAGTCTTCTGTGAACAATGCAATGATATTAACCTTTTATATA	1199

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Oy      1200 AGTT 1203
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Db      1200 AGTT 1203

RESULT 2
US-10-450-826-22
; Sequence 22, Application US/10450826
; Publication No. US20040101818A1
GENERAL INFORMATION:
APPLICANT: Uj, Darren
APPLICANT: Axelrod, Douglas W.
APPLICANT: Cook, Jonathan S.
APPLICANT: Vaiswal, Neelam
APPLICANT: Eistein, Richard
APPLICANT: Houghton, Adam
APPLICANT: Mertz, Lawrence
TITLE OF INVENTION: Gene Expression Profiles Associated with Osteoblast Differentiation
FILE REFERENCE: 040421-5038-WO
CURRENT APPLICATION NUMBER: US/10/450,826
CURRENT FILING DATE: 2003-06-18
PRIOR APPLICATION NUMBER: US 60/255,882
PRIOR FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: US 60/285,691
PRIOR FILING DATE: 2001-04-24
NUMBER OF SEQ ID NOS: 149
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 22
LENGTH: 1203
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Genbank Accession No. X69111
US-10-450-826-22

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Query Match	98.0%;	Score 1178.4;	DB 17;	Length 1203;
Best Local Similarity	99.8%;	Pred. No. 0;		
Matches 1201; Conservative	0;	Mismatches 1;	Indels 2;	Gaps 2

QY	GAATCTGGGGTGTGCTGCACAGAAAAAGCAAAATTTCTGAAAGTTAATGCTTTTGAAGTATCTT	60
Db	1 GATCTGGGGTGTGCTGCACAGAAAAAGCAAAATTTCTGAAAGTTAATGCTTTTGAAGTATTTT	60
QY	61 AAATCTTGTCTGGCGAGAGGCCCGCCCTCTCCCGGATCAGAGGCTTCTCAATCTTTGA	120
Db	61 AAATCTTGTCTGGCGAGAGGCCCGCCCTCTCCCGGATCAGAGGCTTCTCAATCTTTGA	120
QY	121 ATCCGGGGCTCCGCGGCTTTCGGGGTGAACAAGCCGGAGAGAAAGCTGTTTGCAATTTAA	180
Db	121 ATCCGGGGCTCCGCGGCTTTCGGGGTGAACAAGCCGGAGAGAAAGCTGTTTGCAATTTAA	180
QY	181 GCGGGCTGTGAACGCCCAAGGGCGGGCGGGGCGAGGCCAGGCGCATTTTGAAATAA	240
Db	181 GCGGGCTGTGAACGCCCAAGGGCGGGCGGGGCGAGGCCAGGCGCATTTTGAAATAA	240
QY	241 GAGCGGTGCTTTCAGGCAAGGCTCTAATAAGTACCGCGCGCGAGAGCTGTGGCGCGTTC	300
Db	241 GAGCGGTGCTTTCAGGCAAGGCTCTAATAAGTACCGCGCGCGAGAGCTGTGGCGCGTTC	300
QY	301 AGGTACCTGTAAGCGGAATCTTTTGGTTTTCTTTCTTTGGGGCACTCTGAGCTCACT	360
Db	301 AGGTACCTGTAAGCGGAATCTTTTGGTTTTCTTTCTTTGGGGCACTCTGAGCTCACT	360
QY	361 CCCAGCATGAAGGCGCTGAAGCCCGGTGCGCGCTGCTACAGAGGCGGTGTCTACCTGTG	420
Db	361 CCCAGCATGAAGGCGCTGAAGCCCGGTGCGCGCTGCTACAGAGGCGGTGTCTACCTGTG	420
QY	421 GGAACGAGTCTGGCCATGCCCCGGGGCCGAGGAAAGGCCCGGACGTGAGAGCGCGCT	480
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QY	481 GAGCTTCTGAGCAGATGAACAATTGTAATCCCGCGCTGCGGAGACTGGTAACCCGGAGT	540


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Qy 601 CGACCTGACGAGTACTGCTGAGCGAGCAGCCCTGGAACCCCTGTATGGCCCCCACTTCC 660
Db 601 CGACCTGACGAGTACTGCTGAGCGAGCAGCCCTGGAACCCCTGTATGGCCCCCACTTCC 660
Qy 661 CATCCAGACGACGAGCTGCTCCGGAACCTTGTATCTTCCAAAGCAAAAGAGCTTTTG 720
Db 661 CATCCAGACGACGAGCTGCTCCGGAACCTTGTATCTTCCAAAGCAAAAGAGCTTTTG 720
Qy 721 CCACGACTCGGCGCTGCTCTTACACACTTCCAGAAAGCAGAGTGTGGCGCCCTTCTGCT 780
Db 721 CCACGACTCGGCGCTGCTCTTACACACTTCCAGAAAGCAGAGTGTGGCGCCCTTCTGCT 780
Qy 781 GGGACCCCGGGAACCTCTCTGCGGAAAGCGGAGCGGAGTGGGCCCCCACTTCCG 840
Db 781 GGGACCCCGGGAACCTCTCTGCGGAAAGCGGAGCGGAGTGGGCCCCCACTTCCG 840
Qy 841 CTGCCACTTGAATCACTTCAACCAATCCCTTCTGGAAGACTAAACCTGTGCTCAGAGCGAA 900
Db 841 CTGCCACTTGAATCACTTCAACCAATCCCTTCTGGAAGACTAAACCTGTGCTCAGAGCGAA 900
Qy 901 GGAAGTGAATCTTGAAGCTTGAAGAGCCAGAGCTAGCTTGGCCACAGCTGGGAGAGT 960
Db 901 GGAAGTGAATCTTGAAGCTTGAAGAGCCAGAGCTAGCTTGGCCACAGCTGGGAGAGT 960
Qy 961 CACCTGCTCCACCCACCCACCCCAAGTTCTAAGTCTTTTTCAGAGCGGAGTGGAA 1020
Db 961 CACCTGCTCCACCCACCCACCCCAAGTTCTAAGTCTTTTTCAGAGCGGAGTGGAA 1020
Qy 1021 GGAAGTGAATCTTGAAGCTTGAAGAGCCAGAGCTAGCTTGGCTGCTCTT 1080
Db 1021 GGAAGTGAATCTTGAAGCTTGAAGAGCCAGAGCTAGCTTGGCTGCTCTT 1080
Qy 1081 GGAAGTGAATCTTGAAGCTTGAAGAGCCAGAGCTAGCTTGGCTGCTCTT 1139
Db 1081 GGAAGTGAATCTTGAAGCTTGAAGAGCCAGAGCTAGCTTGGCTGCTCTT 1139
Qy 1140 CTTTTCAGAGGAGTACTTCTGTAACAATGGAGTATATTAATTAATTA 1199
Db 1140 CTTTTCAGAGGAGTACTTCTGTAACAATGGAGTATATTAATTAATTA 1199
Qy 1141 CTTTTTAAAGTGAATCTTCTGTAACAATGGAGTATATTAATTAATTA 1199
Db 1141 CTTTTTAAAGTGAATCTTCTGTAACAATGGAGTATATTAATTAATTA 1199
Qy 1200 AGTT 1203
Db 1200 AGTT 1203
Qy 1200 AGTT 1203
Db 1200 AGTT 1203
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; LOCATION: 78, 112, 132, 148, 150, 157, 1405
; OTHER INFORMATION: a, t, c, g, or other
US-10-116-802-341
Query Match 96.8%; Score 1164.2; DB 14, Length 2066;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1199; Conservative 0; Mismatches 3; Indels 3; Gaps 3;
Qy 1 GATCTGGGCTCTGCGAGGAAAGCAATCTGGAATTAATGTTTGTGATGCTT 60
Db 176 GATCTGGGCTCTGCGAGGAAAGCAATCTGGAATTAATGTTTGTGATGCTT 235
Qy 61 AAATCTTGTGCGAGAGCCGCTCTCCCGGATACAGCGCTTCTTCTTGA 120
Db 236 AAATCTTGTGCGAGAGCCGCTCTCTCCCGGATACAGCGCTTCTTCTTGA 295
Qy 121 ATCCGCGCTCCGCGTCTTGGCGTTCAGACAGCCGAGAAAGCTGTTGCAATTTAA 180
Db 236 ATCCGCGCTCCGCGTCTTGGCGTTCAGACAGCCGAGAAAGCTGTTGCAATTTAA 180
Qy 181 GCGGCTGTGAACGCGCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240
Db 236 ATCCGCGCTCCGCGTCTTGGCGTTCAGACAGCCGAGAAAGCTGTTGCAATTTAA 180
Qy 356 GCGGCTGTGAACGCGCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 415
Db 241 GAGGCTGCTTCCAGAGAGCTCTAATAGTACCGCGCGCGCGCGCGCGCGCGCGCG 300
Qy 416 GAGGCTGCTTCCAGAGAGCTCTAATAGTACCGCGCGCGCGCGCGCGCGCGCGCG 475
Db 301 AGGTCTGTAGC-GGACTTCTTTTGTGTTTCTTTTCTTTTGGGCGACTTGAATGAC 359
Qy 476 AGGTCTGTAGCAGGAGCTTCTTTTGTGTTTCTTTTCTTTTGGGCGACTTGAATGAC 535
Db 360 TCCCGAGATGAAGGCGCTGAGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 419
Qy 536 TCCCGAGATGAAGGCGCTGAGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 595
Db 420 CGGAAGCAGTGTGCGCATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 479
Qy 596 CGGAAGCAGTGTGCGCATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 655
Db 480 TGAGCTTGTGAGCAGATGAACCACTGCTTCCCGCGCTGCGGAACTGTATCCCGAG 539
Qy 656 TGAGCTTGTGAGCAGATGAACCACTGCTTCCCGCGCTGCGGAACTGTATCCCGAG 715
Db 540 TCCCGAGAGCAGTGAAGCTTGAAGAGCTTGAAGAGCTTGAAGAGCTTGAAGAG 599
Qy 716 TCCCGAGAGCAGTGAAGCTTGAAGAGCTTGAAGAGCTTGAAGAGCTTGAAGAG 775
Db 600 TCGACCTGAGTACTGCTGCGCGAGCGAGCCCGCTGAGCCCGCTGATGGCCCGCACTTC 659
Qy 776 TCGACCTGAGTACTGCTGCGCGAGCGAGCCCGCTGAGCCCGCTGATGGCCCGCACTTC 835
Db 660 CCATCCAGACAGCCGAGCTGCTCCGGAACCTTGTATCTTCCAAAGCAAAAGAGCTTTT 719
Qy 836 CCATCCAGACAGCCGAGCTGCTCCGGAACCTTGTATCTTCCAAAGCAAAAGAGCTTTT 895
Db 720 GCCACTGACTGCGCGCTGCTGAGACCTTCCAGAAAGCAGAGTGTGCGCGCGCTTCTG 779
Qy 896 GCCACTGACTGCGCGCTGCTGAGACCTTCCAGAAAGCAGAGTGTGCGCGCGCTTCTG 955
Db 780 TGGGACCCCGGGAACCTTCTGCGGAAAGCGGAGCGGAGGAGTGGGCCCCCACTTCC 839
Qy 956 TGGGACCCCGGGAACCTTCTGCGGAAAGCGGAGCGGAGGAGTGGGCCCCCACTTCC 1015
Db 840 CTTGCGCACTTGAATCACTTCAACCAATCCCTTCTGGAAGCTTAACTGTGCTCAGAGCGA 899
Qy 1016 CTTGCGCACTTGAATCACTTCAACCAATCCCTTCTGGAAGCTTAACTGTGCTCAGAGCGA 1075
Db 900 AGGACTGTGAATCTTGTAGCTTGAAGAGCAGAGCTTGTGCGCGCGCGCGCGCGAG 959
Qy 1076 AGGACTGTGAATCTTGTAGCTTGAAGAGCAGAGCTTGTGCGCGCGCGCGCGAG 1135
Db 960 TCACCTGTGCTCCACCCAGCGCGCAAGTTCTAAGGCTTTTTCAGAGCGTGAAGTGTGA 1019
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Db      1136 TACCTGTCTCCACCCCAAGTTCTTAAGTCTTCAAGCGTGAAGTGTGA 1195
Qy      1020 AGAGGTGCTGCTCTCCAAACTATGCGAGCGCGGAGAGCTGTCTTGTCTCT 1079
Db      1196 AGAGGTGCTGCTCTCCAAACTATGCGAGCGCGGAGAGCTGTCTTGTCTCT 1255
Qy      1080 TGAAGAAAGTCTGTGCTCCCTGATTTATGAAGCTTATATAG-GTATATAGTTTTGTA 1138
Db      1256 TGAAGAAAGTCTGTGCTCCCTGATTTATGAAGCTTATATAGTATATAGTTTTGTA 1315
Qy      1139 CTTTTTACAGGAGAGTGACTTTCTGTAACAATGCGATGTATATTTAACTTTTATAA 1198
Db      1316 CTTTTTTACA-GGAAGGTGACTTGTGTATACATGCAATGTATATTTAACTTTTATAA 1374
Qy      1199 AAGTT 1203
Db      1375 AAGTT 1379

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RESULT 4
US-10-084-817-263

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; Sequence 263, Application US/10084817
; Publication No. US20030119009A1
; GENERAL INFORMATION:
; APPLICANT: Susan Stuart
; APPLICANT: Ued G. Nuchtern
; APPLICANT: Sharon E. Pion
; APPLICANT: Jason M. Shohet
; TITLE OF INVENTION: GENES REGULATED BY MYCN ACTIVATION
; FILE REFERENCE: PA-0046 US
; CURRENT FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: US/10/084,817
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 365
; SOFTWARE: PERL Program
; SEQ ID NO 263
; LENGTH: 2066
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030119009A1 253987.19
; LOCATION: 78, 112, 132, 148, 150, 157, 1405
; OTHER INFORMATION: a, c, c, g, or other
US-10-084-817-263

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Query Match 96.8%; Score 1164.2; DB 15; Length 2066;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1199; Conservative 0; Mismatches 3; Indels 3; Gaps 3;

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Qy      1 GATCTGGGGTGTCTGCCAGAAAAGCAATTCTGAGATTATGTTTTGATGATCTT 60
Db      176 GATCTGGGGTGTCTGCCAGAAAAGCAATTCTGAGATTATGTTTTGATGATCTT 235
Qy      61 AAATCTGCTGGGAGAGAGCGCCCTCTCCCGGATATGAGCGCTTCTCATTTCTTGA 120
Db      236 AAATCTGCTGGGAGAGAGCGCCCTCTCCCGGATATGAGCGCTTCTCATTTCTTGA 295
Qy      121 ATCCGCGGTCTCGCGGTCTTTCGCGCTCAGACCAAGCGGAGAGAGCTGTTTGAATTA 180
Db      236 ATCCGCGGTCTCGCGGTCTTTCGCGGTCTCAGACCAAGCGGAGAGAGCTGTTTGAATTA 355
Qy      181 GCGGCTGTGAACGCCACAGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240
Db      356 GCGGCTGTGAACGCCACAGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 415
Qy      241 GAGGCTGCTCTTCCAGGAGAGGCTCTATTAAGTACCGGCGGCGGCGGAGGCTGCGCGCTTGC 300
Db      416 GAGGCTGCTCTTCCAGGAGAGGCTCTATTAAGTACCGGCGGCGGCGGAGGCTGCGCGCTTGC 475

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Qy      301 AGGTCACTGTAGC-GAATCTTTTGTGTTTCTTCTTTGGGCACTCTGTGACTAC 359
Db      476 AGGTCACTGTAGCGGGAATCTTTTGTGTTTCTTCTTTGGGCACTCTGTGACTAC 535
Qy      360 TCCCAAGCATGAGGCGCTGAGCCCGGCTGCGGCTGTCTACGAGCGGTGTGCTGT 419
Db      536 TCCCAAGCATGAGGCGCTGAGCCCGGCTGCGGCTGTCTACGAGCGGTGTGCTGT 595
Qy      420 CGAAGCGAGTGTGAGTTCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 479
Db      596 CGAAGCGAGTGTGAGTTCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 655
Qy      480 TGAAGTCTGTGAGCATGAAACCATCTGACTTCCGCTGCGGGAAGTGGTACCGGAG 539
Db      656 TGAAGTCTGTGAGCATGAAACCATCTGACTTCCGCTGCGGGAAGTGGTACCGGAG 715
Qy      540 TCCGAGAGGACATCAGCTTATGCGAGTGGAAATCTTACAGCGGCTCATGACTACATTG 599
Db      716 TCCGAGAGGACATCAGCTTATGCGAGTGGAAATCTTACAGCGGCTCATGACTACATTG 775
Qy      600 TCGACTGTGAGTGTCTGCGCGAGCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 659
Db      776 TCGACTGTGAGTGTCTGCGCGAGCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 835
Qy      660 CCATTCAGACAGCGGAGCTGCTCCGGAATTTCTTCAACGACAAAGAGCTTTT 719
Db      836 CCATTCAGACAGCGGAGCTGCTCCGGAATTTCTTCAACGACAAAGAGCTTTT 895
Qy      720 GCCACTGACTGCGCGGTCTCTGACACCTGCAAGAGAGGCTGCGGCGGCGGCGGCGGCGGCGG 779
Db      896 GCCACTGACTGCGCGGTCTCTGACACCTGCAAGAGAGGCTGCGGCGGCGGCGGCGGCGGCGG 955
Qy      780 TGGAGCCCGGGAACCTTCTTCCGGAAGCGGAGAGGAGTGGGCGGCACTTCCG 839
Db      956 TGGAGCCCGGGAACCTTCTTCCGGAAGCGGAGAGGAGTGGGCGGCACTTCCG 1015
Qy      840 CTGCGCACTGACTTCAACCAATCCCTTCTGAGAGCTTAACTGTGTCTCAGAGCGA 899
Db      1016 CTGCGCACTGACTTCAACCAATCCCTTCTGAGAGCTTAACTGTGTCTCAGAGCGA 1075
Qy      900 AGGACTGTGAACCTTGTAGCTGTGAAGAGCGAGCTAGCTGTGCGACGAGCGGCGGCGG 959
Db      1076 AGGACTGTGAACCTTGTAGCTGTGAAGAGCGAGCTAGCTGTGCGACGAGCGGCGGCGG 1135
Qy      960 TCAAGCTGCTCCACCCACCCCAAGTCTTAAAGTCTTTTGAAGCTGTGGA 1019
Db      1136 TCAAGCTGCTCCACCCACCCCAAGTCTTAAAGTCTTTTGAAGCTGTGGA 1195
Qy      1020 AGGAGTGTGCTCTCAAACTATGCAAGAGGCGGCGGAGAGCTGTCTTGTGCTCT 1079
Db      1196 AGGAGTGTGCTCTCTCCAACTATGCAAGAGGCGGCGGAGAGCTGTCTTGTGCTCT 1255
Qy      1080 TGAAGAAAGTCTGTGCTCCCTGATTTATGAAGCTTATATAG-GTATATAGTTTTGTA 1138
Db      1256 TGAAGAAAGTCTGTGCTCCCTGATTTATGAAGCTTATATAGTATATAGTTTTGTA 1315
Qy      1139 CTTTTTACAGGAGAGTGACTTTCTGTAACAATGCGATGTATATTTAACTTTTATAA 1198
Db      1316 CTTTTTTACA-GGAAGGTGACTTGTGTATACATGCAATGTATATTTAACTTTTATAA 1374
Qy      1199 AAGTT 1203
Db      1375 AAGTT 1379

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RESULT 5
US-09-925-298-39
; Sequence 39, Application US/09925298
; Publication No. US2002039764A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA103

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/ CURRENT APPLICATION NUMBER: US/09/925,298
/ CURRENT FILING DATE: 2001-08-10
/ PRIOR APPLICATION NUMBER: PCT/US00/05881
/ PRIOR FILING DATE: 2000-03-08
/ PRIOR APPLICATION NUMBER: 60/124,270
/ PRIOR FILING DATE: 1999-03-12
/ NUMBER OF SEQ ID NOS: 846
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 39
/ LENGTH: 1300
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (641)
/ OTHER INFORMATION: n equals a,t,g, or c
/ NAME/KEY: misc_feature
/ LOCATION: (1297)
/ OTHER INFORMATION: n equals a,t,g, or c
/ NAME/KEY: misc_feature
/ LOCATION: (1298)
/ OTHER INFORMATION: n equals a,t,g, or c
/ US-09-925-298-39

Query Match          96.7%; Score 1162.8; DB 9; Length 1300;
Beet Local Similarity 99.1%; Pred. No. 0;
Matches 1194; Conservative 5; Mismatches 3; Indels 3; Gaps 3;

QY      1 GATCTGGGGTGTCTGCCAGGAAAAGCAATTCGTGAAGTTAATGGTTTGAAGTATCTT 60
DB      31 GATCTGGGGTGTCTGCCAGGAAAAGCAATTCGTGAAGTTAATGGTTTGAAGTATCTT 90
QY      61 AATCTCTTGTCTGGCGAGAGGCGCCGCTTCCCGGATACAGCGCTTCTCATTTCTTGA 120
DB      91 AATCTCTTGTCTGGCGAGAGGCGCCGCTTCCCGGATACAGCGCTTCTCATTTCTTGA 150
QY      121 ATCCGGGCTCGCGGGTCTTCCGGCGTCAAGACAGCGGAGAAAGCTGTTTGCATTTAA 180
DB      151 ATCCGGGCTCGCGGGTCTTCCGGCGTCAAGACAGCGGAGAAAGCTGTTTGCATTTAA 210
QY      181 GCGGGCTGTGAAGCGCCAGAGGCGCGGCGGGGCGAGGCGGCGCATTTTGAATATA 240
DB      211 GCGGGCTGTGAAGCGCCAGAGGCGCGGCGGGGCGAGGCGGCGCATTTTGAATATA 270
QY      241 GAGGCGTGTCTTCCAGCGAGGCTCTAATAAGTACCGCGCGCGAGCGTGGCGCGTTC 300
DB      271 GAGGCGTGTCTTCCAGCGAGGCTCTAATAAGTACCGCGCGCGAGCGTGGCGCGTTC 330
QY      301 AGGTACCTGTAGC-GGACTTTTGGTTTCTTCTCTTTGGGGGACCTCTGACTAC 359
DB      331 AGGTACCTGTAGC-GGACTTTTGGTTTCTTCTCTTTGGGGGACCTCTGACTAC 390
QY      360 TCCCGAGCATGAAGGCGTGAAGCGCGGCTGCTGTAACGAGCGGTGTCTGCTGT 419
DB      391 TCCCGAGCATGAAGGCGTGAAGCGCGGCTGCTGTAACGAGCGGTGTCTGCTGT 450
QY      420 CGGAAAGCATGTGTGCGCATGCGCGGGGCGGAGGAAAGGCGCGGAGCTTGAAGAGCGCG 479
DB      451 CGGAAAGCATGTGTGCGCATGCGCGGGGCGGAGGAAAGGCGCGGAGCTTGAAGAGCGCG 510
QY      480 TGAGGCTGTGAGCAAGCAATGCACTGCTACCTCCGCGCTGCGGAACTGTGTAACCGGAG 539
DB      511 TGAGGCTGTGAGCAAGCAATGCACTGCTACCTCCGCGCTGCGGAACTGTGTAACCGGAG 570
QY      540 TCCCGAGAGCACTGAGCTTGAAGCAAGGTGAAATCTTACAGGCGCTGATGACTATTC 599
DB      571 TCCCGAGAGCACTGAGCTTGAAGCAAGGTGAAATCTTACAGGCGCTGATGACTATTC 630
QY      600 TCGACTGTGAGGTAAGTCTGTGGCGAGGCGAGCCCTTGAAGAGGCGGCGGCGGCTTC 659
DB      631 TCGACTGTGAGGTAAGTCTGTGGCGAGGCGAGCCCTTGAAGAGGCGGCGGCGGCTTC 690
QY      660 CCATCCAGACAGCGGAGCTGCGTCCGGAACCTTGTATCTCAACGACAAAGAGCTTTT 719
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DB      691 CCATCCAGACAGCGGAGCTGCGTCCGGAACCTTGTATCTCAACGACAAAGAGCTTTT 750
QY      720 GCCACTGACTGCGCGGTGTCTGACACCTCCAGAAAGCAAGTGTGTGGGCGCGCTTCTGCC 779
DB      751 GCCACTGACTGCGCGGTGTCTGACACCTCCAGAAAGCAAGTGTGTGGGCGCGCTTCTGCC 810
QY      780 TGGGACCGCGGGAACCTCTCCGCGGGAAGCGGACGGGAGGGGCGGCACTTGTGC 839
DB      811 TGGGACCGCGGGAACCTCTCCGCGGGAAGCGGACGGGAGGGGCGGCACTTGTGC 870
QY      840 CCTGCCACTTGACTTCAACCAATCCCTTCTGAGACTAACTGTGTCTGAGAGCGA 899
DB      871 CCTGCCACTTGACTTCAACCAATCCCTTCTGAGACTAACTGTGTCTGAGAGCGA 930
QY      900 AGGACTGTGAACCTGTAGCCTGGAAGAGCGCAAGTACTGTGGCCACGCTGGCGAGC 959
DB      931 AGGACTGTGAACCTGTAGCCTGGAAGAGCGCAAGTACTGTGGCCACGCTGGCGAGC 990
QY      960 TCACCTGTCTCCACCCCAACCCCAAGTTCTTAAGTCTTTTCAAGAGCGGTGAGTGGGA 1019
DB      991 TCACCTGTCTCCACCCCAACCCCAAGTTCTTAAGTCTTTTCAAGAGCGGTGAGTGGGA 1050
QY      1020 AGGACTGTCTCTCAAACTATGCAAGGCGGCGGAGAGCTGTCTGTCTCTCT 1079
DB      1051 AGGACTGTCTCTCTCAAACTATGCAAGGCGGCGGAGAGCTGTCTGTCTCTCTCT 1110
QY      1080 TGGAGAAAGTGTCTGTGCGCTGATTATGAACCTTAATATG-GTATATAGTTTGTGA 1138
DB      1111 TGGAGAAAGTGTCTGTGCGCTGATTATGAACCTTAATATGAGTATATAGTTTGTGA 1170
QY      1139 CTTTTTACAGGGAAGGAGACTTCTGTAACTAAGCATGTATTAACCTTTTATA 1198
DB      1171 CTTTTTACAGGGAAGGAGACTTCTGTAACTAAGCATGTATTAACCTTTTATA 1229
QY      1199 AAGTT 1203
DB      1230 AAGTT 1234

RESULT 6
US-10-102-806-39
/ Sequence 39, Application US/10102806
/ Publication No. US20030054421A1
/ GENERAL INFORMATION:
/ APPLICANT: Rosen et al.
/ TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
/ FILE REFERENCE: P4103P1C1
/ CURRENT APPLICATION NUMBER: US/10/102,806
/ CURRENT FILING DATE: 2002-03-22
/ PRIOR APPLICATION NUMBER: 09/925,298
/ PRIOR FILING DATE: 2001-08-10
/ PRIOR APPLICATION NUMBER: PCT/US00/05881
/ PRIOR FILING DATE: 2000-03-08
/ PRIOR APPLICATION NUMBER: 60/124,270
/ PRIOR FILING DATE: 1999-03-12
/ NUMBER OF SEQ ID NOS: 846
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 39
/ LENGTH: 1300
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (641)
/ OTHER INFORMATION: n equals a,t,g, or c
/ NAME/KEY: misc_feature
/ LOCATION: (1297)
/ OTHER INFORMATION: n equals a,t,g, or c
/ NAME/KEY: misc_feature
/ LOCATION: (1298)
/ OTHER INFORMATION: n equals a,t,g, or c
/ US-10-102-806-39
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Query Match 96.7%; Score 1162.8; DB 14; Length 1300;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 1194; Conservative 5; Mismatches 3; Indels 3; Gaps 3;

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QY 1 GATCTGGAGTGTGTCAGAGAAAGCAAAATTCAGAAAGTAAATGATTTGAGTAACTCT 60
Db 31 GATCTGGAGTGTGTCAGAGAAAGCAAAATTCAGAAAGTAAATGATTTGAGTAACTCT 90
QY 61 AAATCTTGTGAGGAGAGAGGCGGCTCTCTCCGGTATCAGGCTCTCTCATTTCTTGA 120
Db 91 AAATCTTGTGAGGAGAGAGGCGGCTCTCTCCGGTATCAGGCTCTCTCATTTCTTGA 150
QY 121 ATCCGCGGCTCCGGGCTTTTCGGGTCAAGACAGCCGAGAGAGGCTTTGCAATTTA 180
Db 151 ATCCGCGGCTCCGGGCTTTTCGGGTCAAGACAGCCGAGAGAGGCTTTGCAATTTA 210
QY 181 GCGGGCTGTGAACCCCAAGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240
Db 211 GCGGGCTGTGAACCCCAAGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 270
QY 241 GAGCGTGTGCTTCAGGAGAGGCTCTATAGTAAACCGCGCGGAGAGAGCTTCGGCGTTC 300
Db 271 GAGCGTGTGCTTCAGGAGAGGCTCTATAGTAAACCGCGCGGAGAGCTTCGGCGTTC 330
QY 301 AGGTCACTGTAGC-GGACTTTTGTGTTTCTTTCTTTTGGGCGACCTGTGACTGAC 359
Db 331 AGGTCACTGTAGCAGGAGGCTTTTGTGTTTCTTTCTTTTGGGCGACCTGTGACTGAC 390
QY 360 TCCCGAGAGAGAGGCGGCTGAGCGCGGCTGCGCGGCTGCTACAGAGCGGTGCTGCTGT 419
Db 391 TCCCGAGAGAGAGGCGGCTGAGCGCGGCTGCGCGGCTGCTACAGAGCGGTGCTGCTGT 450
QY 420 CGAAGCGAGTGTGCGCATGCGCGGCGGCGAGAGAGAGAGAGAGAGAGAGAGAGAG 479
Db 451 CGAAGCGAGTGTGCGCATGCGCGGCGGCGAGAGAGAGAGAGAGAGAGAGAGAGAG 510
QY 480 TGAAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 539
Db 511 TGAAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 570
QY 540 TCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 599
Db 571 TCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 630
QY 600 TCGAAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 659
Db 631 TCGAAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 690
QY 660 CCATCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 719
Db 691 CCATCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 750
QY 720 GCGAAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 779
Db 751 GCGAAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 810
QY 780 TGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 839
Db 811 TGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 870
QY 840 CCGTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 899
Db 871 CCGTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 930
QY 900 AGGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 959
Db 931 AGGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 990
QY 960 TCAAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1019
Db 991 TCAAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1050
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QY 1020 AGGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1079
Db 1051 AGGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1110
QY 1080 TGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1138
Db 1111 TGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1170
QY 1139 CCGTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1198
Db 1171 CCGTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1229
QY 1199 AAGTT 1203
Db 1230 AAGTT 1234
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RESULT 7

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US-10-198-846-13483
; Sequence 13483, Application US/10198846
; Publication No. US2003009974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steinhilber, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198, 846
; PRIOR APPLICATION NUMBER: 2002-07-18
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 13483
; LENGTH: 1504
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 1497, 1498, 1499, 1500, 1501, 1502, 1503, 1504
; OTHER INFORMATION: n = A,T,C or G
US-10-198-846-13483
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Query Match 79.0%; Score 950.8; DB 14; Length 1504;
Best Local Similarity 97.4%; Pred. No. 7; 5e-294;
Matches 1009; Conservative 0; Mismatches 22; Indels 5; Gaps 4;

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QY 170 TTGCAATTTAAGCGGCTGTGAAAGCCCAAGAGCGCGGCGGCGGCGGCGGCGCA 229
Db 11 TTGCAATTTAAGCGGCTGTGAAAGCCCAAGAGCGCGGCGGCGGCGGCGGCGCA 70
QY 230 TTTTGAATTAAGAGCGGCTGTGAAAGCGGCTGTATATAGTAAACCGCGGAGAGGT 289
Db 71 TTTTGAATTAAGAGAGCAATTTTC-ACGAGAGAGAGTATTAAGAGAGAGAGAGGT 128
QY 290 GGGCGGCTTGCAGGCTGATGTAGC-GGACTTTTGTGTTTCTTTCTTTTGGGAGAC 348
Db 129 GGGCGGCTTGCAGGCTGATGTAGCAGGACTTTTGTGTTTCTTTCTTTTGGGAGAC 188
QY 349 TGTGACTCACTCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 408
Db 189 TGTGACTCACTCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 248
QY 409 GTGCTGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 468
Db 249 GTGCTGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 308
QY 469 TGAAGAGCGGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 528
Db 309 TGAAGAGCGGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 368
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QY 529 GGTACCCGAGTCCCGAGAGCACTCAGCTTAGCCAGTGAATCTCAGCGGTGAT 588
DB 369 GGTACCCGAGTCCCGAGAGCACTCAGCTTAGCCAGTGAATCTCAGCGGTGAT 428
QY 589 GCACTACATCTCGACTGAGCTGAGTACTCTGCGGAGCCAGCCCTGAGCCCCGTGATG 648
DB 429 GCACTACATCTCGACTGAGCTGAGTACTCTGCGGAGCCAGCCCTGAGCCCCGTGATG 488
QY 649 CCCCCACCTTCCCATTCACACAGCCGAGCTCGTCCGGAATTGTCACTTCCAGACAA 708
DB 489 CCCCCACCTTCCCATTCACACAGCCGAGCTCGTCCGGAATTGTCACTTCCAGACAA 548
QY 709 AAGAGCTTTTGACACTGACTCGGCGGTGCTGACACCTCCAGAAAGCAGGAGCTGAG 768
DB 549 AAGAGCTTTTGACACTGACTCGGCGGTGCTGACACCTCCAGAAAGCAGGAGCTGAG 608
QY 769 CCGGTTCTGCTGGGAGCCCGGGAACCTCTCTGCGGAAAGCCGAGCGGAGGATGAGC 828
DB 609 CCGGTTCTGCTGGGAGCCCGGGAACCTCTCTGCGGAAAGCCGAGCGGAGGATGAGC 668
QY 829 CCGAATTGCGCCCTGCGGCACTTGAATTCACCAATCCCTTCTGAGACTAAACCTGAGT 888
DB 669 CCGAATTGCGCCCTGCGGCACTTGAATTCACCAATCCCTTCTGAGACTAAACCTGAGT 728
QY 889 CTCAGAGGAGAGAGCTGTGAACCTGTAGCTGAGAGAGCCAGAGCTAGCTGAGCCAGCA 948
DB 729 CTCAGAGGAGAGAGCTGTGAACCTGTAGCTGAGAGAGCCAGAGCTAGCTGAGCCAGCA 788
QY 949 GCTGGGCGAGCTGACCTGCTGCTCCACCCAGCCCAAGTTCTTAAGTCTTTTCAGAGCT 1008
DB 789 GCTGGGCGAGCTGACCTGCTGCTCCACCCAGCCCAAGTTCTTAAGTCTTTTCAGAGCT 848
QY 1009 GGAAGTGTGAAGAGAGTGGCTGCTCTCCAACTATGCTCAAGGCGGCGAGAGCTGCT 1068
DB 849 GGAAGTGTGAAGAGAGTGGCTGCTCTCCAACTATGCTCAAGGCGGCGAGAGCTGCT 908
QY 1069 TCTGGCTCTTGAAGAGAGTTCTGTGCCGATTTATGAATCTTAATAG-CTAAT 1127
DB 909 TCTGGCTCTTGAAGAGAGTTCTGTGCCGATTTATGAATCTTAATAGAGTATA 968
QY 1128 TAGGTTTGTACCTTTTTCACAGAGAGTGACTTCTGTAACTATGATATTTAA 1187
DB 969 TAGGTTTGTACCTTTTTCAC- GGAAGGTGACTTCTGTAACTATGATATTTAA 1027
QY 1188 ACTTTTATATAAGTT 1203
DB 1028 ACTTTTATATAAGTT 1043

RESULT 8
US-10-450-826-21
; Sequence 21, Application US/10450826
; Publication No. US20040101818A1
; GENERAL INFORMATION:
; APPLICANT: JI, Darren
; APPLICANT: Axelrod, Douglas W.
; APPLICANT: Cook, Jonathan S.
; APPLICANT: Jaiswal, Neelam
; APPLICANT: Eistein, Richard
; APPLICANT: Houghton, Adam
; APPLICANT: Metz, Lawrence
; TITLE OF INVENTION: Gene Expression Profiles Associated with Osteoblast Differentiat
; FILE REFERENCE: 044921-5039-WO
; CURRENT APPLICATION NUMBER: US/10/450,826
; PRIOR FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: US 60/255,882
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 60/285,691
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 21

; LENGTH: 982
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. X66924
US-10-450-826-21
Query Match 71.2%; Score 856.2; DB 17; Length 982;
Best Local Similarity 97.7%; Pred. No. 1.4e-263;
Matches 900; Conservative 0; Mismatches 18; Indels 3; Gaps 3;
QY 284 GAGCGTGGCGCGGTGACAGTCACTGAGCGGACTTCTTTGTTTCTTTCTTTGGG 343
DB 40 GATCTGACACACGGGAACTCAGACAGCTCACTTCTTTGTTTCTTTCTTTGGG 99
QY 344 GCACTCTGAGTCACTCTCCACGATGAAGCGCTGAGGCCGCTGCGCTGCTACGAG 403
DB 100 GCACCTCTGAGTCACTCTCCACGATGAAGCGCTGAGGCCGCTGCGCTGCTACGAG 159
QY 404 GCGGTGCTGCTGCTGCGGAAACGAGCTGCGCACTGCGCGGCGGAGGAGGCGCG 463
DB 160 GCGGTGCTGCTGCTGCGGAAACGAGCTGCGCACTGCGCGGCGGAGGAGGCGCG 219
QY 464 GCGCTGAGAGAGCGCTGAGCTTGTGAGCAGATGAACCACTGCTACTCCGCGCTGCG 523
DB 220 GCGCTGAGAGAGCGCTGAGCTTGTGAGCAGATGAACCACTGCTACTCCGCGCTGCG 279
QY 524 GAACTGTGACCCGAGAGTCCGAGAGGCACTCAGCTTAAAGCAGGTGAAATCTTACAGCGC 583
DB 280 GAACTGTGACCCGAGAGTCCGAGAGGCACTCAGCTTAAAGCAGGTGAAATCTTACAGCGC 339
QY 584 GTGATGACTGACTATCTGACCTGAGAGTATGCTGCGGAGCCAGCCCTGAGACCCCT 643
DB 340 GTGATGACTGACTATCTGACCTGAGAGTATGCTGCGGAGCCAGCCCTGAGACCCCT 399
QY 644 GATGAGCCCACTTCCCATCCAGACAGCCGAGCTGCTCCGGAATTGTCTTCAAC 703
DB 400 GATGAGCCCACTTCCCATCCAGACAGCCGAGCTGCTCCGGAATTGTCTTCAAC 459
QY 704 GACAAAGAGCTTTTTCACAGTCACTGAGCTGAGCTGCTGAGCACTTCCAGAACGAGTGC 763
DB 460 GACAAAGAGCTTTTTCACAGTCACTGAGCTGAGCTGAGCTGAGCACTTCCAGAACGAGTGC 519
QY 764 TGGCGCCGCTTCTGCTGAGAGCCCGGGAACCTCTCTGCGGAGCCGGAAGCGGAGGGA 823
DB 520 TGGCGCCGCTTCTGCTGAGAGCCCGGGAACCTCTCTGCGGAGCCGGAAGCGGAGGGA 579
QY 824 TGGCGCCCAACTTCCGCTGAGCTTCACTTCACTTCACTTCACTTCACTTCACTTCA 883
DB 580 TGGCGCCCAACTTCCGCTGAGCTTCACTTCACTTCACTTCACTTCACTTCACTTCA 639
QY 884 TGGCTCTGAGAGCGAGAGAGCTGTGAACCTTGTAGCTTGAAGAGCGAGAGCTAGCTGAGC 943
DB 640 TGGCTCTGAGAGCGAGAGAGCTGTGAACCTTGTAGCTTGAAGAGCGAGAGCTAGCTGAGC 699
QY 944 CACGAGCTGGGAGAGTCACTCTGCTCCACCCCAAGTTCTTAAGTCTTTTCAAG 1003
DB 700 CACGAGCTGGGAGAGTCACTCTGCTCCACCCCAAGTTCTTAAGTCTTTTCAAG 758
QY 1004 AGCGTGAAGTGTGAAGAGAGTGTGCTCTTCAACTATGCGAGAGCGGCGGAGAGCT 1063
DB 759 AGCGTGAAGTGTGAAGAGAGTGTGCTCTTCAACTATGCGAGAGCGGCGGAGAGCT 818
QY 1064 GGTCTTCTGCTCTCTTGAAGAGAGTTCTGTGCTGATTTATGAATCTTATATAG- 1122
DB 819 GGTCTTCTGCTCTCTTGAAGAGAGTTCTGTGCTGATTTATGAATCTTATATAG 878
QY 1123 GTATATAGTTTGTGACTTTTTCACAGGAGAGTGAATTTCTGTAACTATGATAT 1182
DB 879 GTATATAGTTTGTGACTTTTTCAC- GGAAGGTGACTTCTGTAACTATGATAT 937
QY 1183 ATTAACCTTTTATATAAGTT 1203

Db 938 ATTAACCTTTTATTAAGTT 938

RESULT 9
US-10-450-826-23

/ Sequence 23, Application US/10450826
/ Publication No. US2004010181A1

/ GENERAL INFORMATION:

/ APPLICANT: J1, Darren

/ APPLICANT: Axelrod, Douglas W.

/ APPLICANT: Cook, Jonathan S.

/ APPLICANT: Jaiswal, Neelam

/ APPLICANT: Eistein, Richard

/ APPLICANT: Houghton, Adam

/ APPLICANT: Metz, Lawrence

/ TITLE OF INVENTION: Gene Expression Profiles Associated with Osteoblast Differentiat

/ FILE REFERENCE: 044921-5039-WO

/ CURRENT APPLICATION NUMBER: US/10/450,826

/ CURRENT FILING DATE: 2003-06-18

/ PRIOR APPLICATION NUMBER: US 60/255,882

/ PRIOR FILING DATE: 2000-12-18

/ PRIOR APPLICATION NUMBER: US 60/285,691

/ PRIOR FILING DATE: 2001-04-24

/ NUMBER OF SEQ ID NOS: 149

/ SOFTWARE: Patent Ver. 2.1

/ SEQ ID NO 23

/ LENGTH: 2481

/ TYPE: DNA

/ ORGANISM: Homo sapiens

/ OTHER INFORMATION: Genbank Accession No. X73428

US-10-450-826-23

Query Match 55.2%; Score 663.8; DB 17; Length 2481;
Best Local Similarity 99.7%; Pred. No. 1.2e-201;
Matches 665; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GATCTGGGCTGCTCCAGGAGAAAGCAATTCTGGAAGTTAATGTTTGAATGATTTCTT 60
DB 372 GATCTGGGCTGCTCCAGGAGAAAGCAATTCTGGAAGTTAATGTTTGAATGATTTCTT 431
QY 61 AAATCTTCTGCTGCGAGAGAGCCCGCTCTCCCGGTATCAGCGCTTCTCTATTCTTTGA 120
DB 432 AAATCTTCTGCTGCGAGAGAGCCCGCTCTCCCGGTATCAGCGCTTCTCTATTCTTTGA 491
QY 121 ATCCGCGGCTCCGCGGTCTTCCGCTCAACAAGCCGAGAGAGAGCTGTTTGCATTTAA 180
DB 492 ATCCGCGGCTCCGCGGTCTTCCGCTCAACAAGCCGAGAGAGAGCTGTTTGCATTTAA 551
QY 181 GCGGGCTGTAAGAGCCAGGAGCCGCGGGGCGGGGCGAGGCGGAGCATTTTGAATTA 240
DB 552 GCGGGCTGTAAGAGCCAGGAGCCGCGGGGCGGGGCGAGGCGGAGCATTTTGAATTA 611
QY 241 GAGGCGTGCCTTCCAGGAGAGCTCTAATAGTGAAGCCGCGGAGAGCTGCGCGCTTGC 300
DB 612 GAGGCGTGCCTTCCAGGAGAGCTCTAATAGTGAAGCCGCGGAGAGCTGCGCGCTTGC 671
QY 301 AGGTCACTGAAGCGAATTTTGGTTTCTTCTTCTTGGGAGCACTCTGAGACTCACT 360
DB 672 AGGTCACTGAAGCGAATTTTGGTTTCTTCTTCTTGGGAGCACTCTGAGACTCACT 731
QY 361 CCCGAGATGAAGAGCGCTGAGCGGCTGAGCGCTGAGAGCGGAGCTGAGCGCTGCTGTC 420
DB 732 CCCGAGATGAAGAGCGCTGAGCGGCTGAGCGGCTGAGAGCGGAGCTGAGCGCTGCTGTC 791
QY 421 GGAAGCGAGCTGAGCGCTGAGCGGCTGAGCGGCTGAGAGCGGAGCTGAGCGCTGCTGTC 480
DB 792 GGAAGCGAGCTGAGCGCTGAGCGGCTGAGCGGCTGAGAGCGGAGCTGAGCGCTGCTGTC 851
QY 481 GAGCTTCTGAGAGCAATGAACACTGCTAATCCCGCTGAGGAGAGCTGCTGAGCGGAGT 540
DB 852 GAGCTTCTGAGAGCAATGAACACTGCTAATCCCGCTGAGGAGAGCTGCTGAGCGGAGT 911

QY 541 CCCGAGAGCACTCAGCTTAGCCAGGTGAAATCTTACAGCGGCTGATGACTATCTTCT 600
DB 912 CCCGAGAGCACTCAGCTTAGCCAGGTGAAATCTTACAGCGGCTGATGACTATCTTCT 971
QY 601 CGACTGCAAGTATCTTGGCCGAGCCAGCCCTGAGCCCTGATGAGCCCACTTCTCC 660
DB 972 CGACTGCAAGTATCTTGGCCGAGCCAGCCCTGAGCCCTGATGAGCCCACTTCTCC 1031
QY 661 CATCCAG 667
DB 1032 CATCCAG 1038

RESULT 10
US-10-450-826-24/C

/ Sequence 24, Application US/10450826
/ Publication No. US2004010181A1

/ GENERAL INFORMATION:

/ APPLICANT: J1, Darren

/ APPLICANT: Axelrod, Douglas W.

/ APPLICANT: Cook, Jonathan S.

/ APPLICANT: Jaiswal, Neelam

/ APPLICANT: Eistein, Richard

/ APPLICANT: Houghton, Adam

/ APPLICANT: Metz, Lawrence

/ TITLE OF INVENTION: Gene Expression Profiles Associated with Osteoblast Differentiat

/ FILE REFERENCE: 044921-5039-WO

/ CURRENT APPLICATION NUMBER: US/10/450,826

/ CURRENT FILING DATE: 2003-06-18

/ PRIOR APPLICATION NUMBER: US 60/255,882

/ PRIOR FILING DATE: 2000-12-18

/ PRIOR APPLICATION NUMBER: US 60/285,691

/ PRIOR FILING DATE: 2001-04-24

/ NUMBER OF SEQ ID NOS: 149

/ SOFTWARE: Patent Ver. 2.1

/ SEQ ID NO 24

/ LENGTH: 129722

/ TYPE: DNA

/ ORGANISM: Homo sapiens

/ OTHER INFORMATION: Genbank Accession No. AL021154

US-10-450-826-24

Query Match 54.3%; Score 652.8; DB 17; Length 129722;
Best Local Similarity 99.6%; Pred. No. 2.3e-197;
Matches 665; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 GATCTGGGCTGCTCCAGGAGAAAGCAATTCTGGAAGTTAATGTTTGAATGATTTCTT 60
DB 109558 GATCTGGGCTGCTCCAGGAGAAAGCAATTCTGGAAGTTAATGTTTGAATGATTTCTT 109499
QY 61 AAATCTTCTGCTGCGAGAGAGCCCGCTCTCCCGGTATCAGCGCTTCTCTATTCTTTGA 120
DB 109498 AAATCTTCTGCTGCGAGAGAGCCCGCTCTCCCGGTATCAGCGCTTCTCTATTCTTTGA 109439
QY 121 ATCCGCGGCTCCGCGGTCTTCCGCTCAACAAGCCGAGAGAGAGCTGTTTGCATTTAA 180
DB 109438 ATCCGCGGCTCCGCGGTCTTCCGCTCAACAAGCCGAGAGAGAGCTGTTTGCATTTAA 109379
QY 181 GCGGGCTGTAAGCCAGGAGCCGCGGGGCGGGGCGAGGCGGAGCATTTTGAATTA 240
DB 109378 GCGGGCTGTAAGCCAGGAGCCGCGGGGCGGGGCGAGGCGGAGCATTTTGAATTA 109319
QY 241 GAGGCGTGCCTTCCAGGAGAGCTCTAATAGTGAAGCCGCGGAGAGCTGCGCGCTTGC 300
DB 109318 GAGGCGTGCCTTCCAGGAGAGCTCTAATAGTGAAGCCGCGGAGAGCTGCGCGCTTGC 109259
QY 301 AGGTCACTGAAGCGAATTTTGGTTTCTTCTTCTTGGGAGCACTCTGAGACTCAC 359
DB 109258 AGGTCACTGAAGCGGAGATTTTGGTTTCTTCTTCTTGGGAGCACTCTGAGACTCAC 109199
QY 360 TCCCGAGATGAAGCGCTGAGCCCGGCTGCTAAGAGCGGCTGCTAAGAGCGGCTGCTGT 419

Db 109198 TCCCCAGATGAAAGCGCTGAGCCCGGCTGCTACGAGCGGTGCTGCTCTGT 109139
Qy 420 CGGAACGAGTGTGCGCAATTCGGCCGGCGGAGGAAAGGCGCCGAGCTGAGAGCCGC 479
Db 109138 CGGAACGAGTGTGCGCAATTCGGCCGGCGGAGGAAAGGCGCCGAGCTGAGAGCCGC 109079
Qy 480 TGAGCTTGCTGAGACGACATGAAACAATGCTACTCCCGCTGCGGGAATGTAACCCGAG 539
Db 109078 TGAGCTTGCTGAGACGACATGAAACAATGCTACTCCCGCTGCGGGAATGTAACCCGAG 109019
Qy 540 TCCGAGAGGACCTAGCTTACCGAGGTGAATCTTACAGGCGGTCACTGATTC 599
Db 109018 TCCGAGAGGACCTAGCTTACCGAGGTGAATCTTACAGGCGGTCACTGATTC 108959
Qy 600 TCGACCTGAGAGTACTGCTGCGGAGCCGCGCCCTGAGACCCCTGATGAGCCCACTTC 659
Db 108958 TCGACCTGAGAGTACTGCTGCGGAGCCGCGCCCTGAGACCCCTGATGAGCCCACTTC 108899
Qy 660 CCATCCAG 667
Db 108898 CCATCCAG 108891

RESULT 11

US-09-919-039-214
; Sequence 214, Application US/09919039
; Publication No. US20030108871A1
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 214
; LENGTH: 653
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030108871A1 253987.16
US-09-919-039-214

Query Match 36.4%; Score 437.8; DB 10; Length 653;

Best Local Similarity 97.2%; Pred. No. 2,1e-129;

Matches 456; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

Qy 736 TGTCTGACACCTCCAGAAAGGAGTGTGCGCCCGCTTCTGCTGAGACCCCGGAAAC 795
Db 147 TTTCTCTCCCGCCCGCAGAAAGGAGTGTGCGCCCGCTTCTGCTGAGACCCCGGAAAC 206
Qy 796 TGTCTGACACCTCCAGAAAGGAGTGTGCGCCCGCTTCTGCTGAGACCCCGGAAAC 855
Db 207 TGTCTGACACCTCCAGAAAGGAGTGTGCGCCCGCTTCTGCTGAGACCCCGGAAAC 266
Qy 856 CACCAATCCCTTCTGAGACTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTG 915
Db 267 CACCAATCCCTTCTGAGACTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTG 326
Qy 916 AGCTGAGAGCGCAGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTG 975
Db 327 GGCCTGAGAGCGCAGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTG 386
Qy 976 CACACCCCAAGTCTTAAGGCTTTTCAAGCGTGAAGCGTGAAGCGTGAAGCGTGAAG 1035
Db 387 CACACCCCAAGTCTTAAGGCTTTTCAAGCGTGAAGCGTGAAGCGTGAAGCGTGAAG 446
Qy 1036 CAAACTATGCTCAAGCGCGGCGGAGAGCTGCTTCTGCTGCTGCTGAGAAAGTTCTGT 1095
Db 447 CAAACTATGCTCAAGCGCGGCGGAGAGCTGCTGCTGCTGCTGCTGAGAAAGTTCTGT 506

Qy 1096 TGCCCTGATTTATGAACTCTAATAAG-GTATATAGTTTTGTACCTTTTACAGGGA 1154
Db 507 TGCCCTGATTTATGAACTCTAATAAG-GTATATAGTTTTGTACCTTTTACAGGGA 566
Qy 1155 GGTGACTTTCTGTAACTATGAGATGATATTAATTAATTTTATTAAGTT 1203
Db 567 GGTGACTTTCTGTAACTATGAGATGATATTAATTAATTTTATTAAGTT 615

RESULT 12

US-10-116-802-341/c
; Sequence 341, Application US/10116802
; Publication No. US20030065157A1
; GENERAL INFORMATION:
; APPLICANT: Amy Laesk
; TITLE OF INVENTION: GENES EXPRESSED IN LUNG CANCER
; FILE REFERENCE: PA-0045 US
; CURRENT APPLICATION NUMBER: US/10/116,802
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 60/281,593
; PRIOR FILING DATE: 2001-04-04
; NUMBER OF SEQ ID NOS: 519
; SOFTWARE: PERL Program
; SEQ ID NO 341
; LENGTH: 2066
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 253987.19
; NAME/KEY: unsure
; LOCATION: 78, 112, 132, 148, 150, 157, 1405
; OTHER INFORMATION: a, t, c, g, or other
US-10-116-802-341

Query Match 36.4%; Score 437.8; DB 14; Length 2066;

Best Local Similarity 97.2%; Pred. No. 3,5e-129;

Matches 456; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

Qy 736 TGTCTGACACCTCCAGAAAGGAGTGTGCGCCCGCTTCTGCTGAGACCCCGGAAAC 795
Db 1920 TTTCTCTCCCGCCCGCAGAAAGGAGTGTGCGCCCGCTTCTGCTGAGACCCCGGAAAC 1861
Qy 796 TGTCTGACACCTCCAGAAAGGAGTGTGCGCCCGCTTCTGCTGAGACCCCGGAAAC 855
Db 1860 TGTCTGACACCTCCAGAAAGGAGTGTGCGCCCGCTTCTGCTGAGACCCCGGAAAC 1801
Qy 856 CACCAATCCCTTCTGAGACTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTG 915
Db 1800 CACCAATCCCTTCTGAGACTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTG 1741
Qy 916 AGCTGAGAGCGCAGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTG 975
Db 1740 GGCCTGAGAGCGCAGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTG 1681
Qy 976 CACACCCCAAGTCTTAAGGCTTTTCAAGCGTGAAGCGTGAAGCGTGAAGCGTGAAG 1035
Db 1680 CACACCCCAAGTCTTAAGGCTTTTCAAGCGTGAAGCGTGAAGCGTGAAGCGTGAAG 1621
Qy 1036 CAAACTATGCTCAAGCGCGGCGGAGAGCTGCTTCTGCTGCTGCTGAGAAAGTTCTGT 1095
Db 1620 CAAACTATGCTCAAGCGCGGCGGAGAGCTGCTTCTGCTGCTGCTGAGAAAGTTCTGT 1561
Qy 1096 TGCCCTGATTTATGAACTCTAATAAG-GTATATAGTTTTGTACCTTTTACAGGGA 1154
Db 1560 TGCCCTGATTTATGAACTCTAATAAG-GTATATAGTTTTGTACCTTTTACAGGGA 1501
Qy 1155 GGTGACTTTCTGTAACTATGAGATGATATTAATTAATTTTATTAAGTT 1203
Db 1500 GGTGACTTTCTGTAACTATGAGATGATATTAATTAATTTTATTAAGTT 1452


```
RESULT 13
US-10-084-817-263/c
; Sequence 263, Application US/10084817
; Publication No. US2003011909A1
; GENERAL INFORMATION:
; APPLICANT: Susan Stuart
; APPLICANT: Jed G. Nuchtern
; APPLICANT: Sharon E. Plon
; APPLICANT: Jason M. Shohet
; TITLE OF INVENTION: GENES REGULATED BY MYCN ACTIVATION
; FILE REFERENCE: PA-0046 US
; CURRENT FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 60/270,784
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 365
; SOFTWARE: PERL Program
; SEQ ID NO 263
; LENGTH: 2066
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US2003011909A1 253987.19
; LOCATION: 78, 112, 132, 148, 150, 157, 1405
; OTHER INFORMATION: a, t, c, g, or other
US-10-084-817-263

Query Match      36.4%; Score 437.8; DB 15; Length 2066;
Best Local Similarity 97.2%; Fred. No. 3.5e-129;
Matches 455; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

QY      736 TGTCGACACCTCCAGAAAGCAGTGTGCGCCGCTTCTGCTGGAGCCCGGGAACC
DB      1920 TTTCCTCCCGCCCGGAGAGAGAGTGTGCGCCGCTTCTGCTGGAGCCCGGGAACC
QY      796 TCTCTGCGGGAAGCGGAGCGAGGATGGGCCCCCACTTGCCTGCGCCACTTGACTT
DB      1860 TCTCTGCGGGAAGCGGAGCGAGGATGGGCCCCCACTTGCCTGCGCCACTTGACTT
QY      856 CACCAATCCCTTCTGAGACTTAACTGCTGCTCAGAGAGGAGAGTGAACCTTGT
DB      1800 CACCAATCCCTTCTGAGACTTAACTGCTGCTCAGAGAGGAGAGTGAACCTTGT
QY      916 AGCTGGAAGGCGAAGCTAGCTGTGCGCACCGAGTGGGCAAGTCACTGCTCCAGC
DB      1740 GGCCTGGAAGGCGAAGCTAGCTGTGCGCACCGAGTGGGCAAGTCACTGCTCCAGC
QY      976 CCACCCCAAGTCTTAAGTCTTTTCAAGAGCTGGAAGTGGAGAGTGGCTCTC
DB      1680 CCACCCCAAGTCTTAAGTCTTTTCAAGAGCTGGAAGTGGAGAGTGGCTCTC
QY      1036 CAAACTATGCGAAGCGCGGCGAGAGCTGTCTTCTGCTCTCTTGGAGAAAGTCTGT
DB      1620 CAAACTATGCGAAGCGCGGCGAGAGCTGTCTTCTGCTCTCTTGGAGAAAGTCTGT
QY      1096 TGCCTGATTTATGAACTCTATATAG- GATATAGTTTGTACTTTTTCAGGGAA
DB      1560 TGCCTGATTTATGAACTCTATATAG- GATATAGTTTGTACTTTTTCAGGGAA
QY      1155 GGTGACTTCTGTACATGAGATGATATTAACCTTTTAAAGTT 1203
DB      1500 GGTGACTTCTGTACATGAGATGATATTAACCTTTTAAAGTT 1452

RESULT 14
US-09-918-995-31450
; Sequence 31450, Application US/09918995
; Publication No. US2003007623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
```

```
; FILE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 31450
; LENGTH: 465
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(465)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-31450

Query Match      35.3%; Score 425; DB 10; Length 465;
Best Local Similarity 100.0%; Fred. No. 2.3e-125;
Matches 425; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      347 CCTGTGACACACCTCCAGCATGAAGGCGCTGAGCCCGGTGCGCGCTGCTACAGGCG
DB      41 CCTGTGACACACCTCCAGCATGAAGGCGCTGAGCCCGGTGCGCGCTGCTACAGGCG
QY      407 GTGTGCTGCTGTGGAAGCAGTGTGCGCCATGCGCCGGGCGGAGAGGCGCGGCA
DB      101 GTGTGCTGCTGTGGAAGCAGTGTGCGCCATGCGCCGGGCGGAGAGGCGCGGCA
QY      467 GCTGAGAGCGCGTGAAGCTGCTGAGACATGAACACTGCTACTCTCCGCTGCGGAA
DB      161 GCTGAGAGCGCGTGAAGCTGCTGAGACATGAACACTGCTACTCTCCGCTGCGGAA
QY      527 CTGTACCCGAGATCCCGAGAGGCACTCAGCTTAGCGAGTGAATCTTACAGCGCTTC
DB      221 CTGTACCCGAGATCCCGAGAGGCACTCAGCTTAGCGAGTGAATCTTACAGCGCTTC
QY      587 ATGACTACATTTGACCTGACAGTATGCTTGGCCGAGCCAGCCCTGGAACCCCTGAT
DB      281 ATGACTACATTTGACCTGACAGTATGCTTGGCCGAGCCAGCCCTGGAACCCCTGAT
QY      647 GGGCCCACTTCCATCCAGACAGCGGAGCTCGCTCCGGAACTTGTCACTCCAGAC
DB      341 GGGCCCACTTCCATCCAGACAGCGGAGCTCGCTCCGGAACTTGTCACTCCAGAC
QY      707 AAAAGAGCTTTTCCACTGACTCGGCGGTGCTGACACTCCAGAAAGAGGTGTG
DB      401 AAAAGAGCTTTTCCACTGACTCGGCGGTGCTGACACTCCAGAAAGAGGTGTG
QY      767 CGGCC 771
DB      461 CGGCC 465

RESULT 15
US-09-918-995-8760
; Sequence 8760, Application US/09918995
; Publication No. US2003007623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8760
; LENGTH: 429
; TYPE: DNA
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ORGANISM: Homo sapiens
US-09-918-8760

Query Match 35.1%; Score 422.6; DB 10; Length 429;
Best Local Similarity 99.1%; Pred. No. 1.3e-124;
Matches 425; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY	315	GACCTCTTTTGGTTCTTTCTTTGGGGGACCTGTGGACCTGAGACTACCTCCCGACATGAAGG	374
DB	1	GACCTCTTTTGGTTCTTTCTTTGGGGGACCTGTGGACCTGAGACTACCTCCCGACATGAAGG	60
QY	375	CGCTAGCCCGGGTGGCGCGGCTGCTAGAGCGGTTGCTGCTGTGGAACGCACTTGG	434
DB	61	CGCTAGCCCGGGTGGCGCGGCTGCTAGAGCGGTTGCTGCTGTGGAACGCACTTGG	120
QY	435	CCATGCGCCGGGGCCGAGGGGAAGGGCCCGGCACTGAGGAGCCGCTGAGCTTGTGGAAG	494
DB	121	CCATGCGCCGGGGCCGAGGGGAAGGGCCCGGCACTGAGGAGCCGCTGAGCTTGTGGAAG	180
QY	495	ACATGAACCACTGCTACTCCCGGCTGGCGGGAAGTGTACCCGGAGTCCCGAGAGGCACTC	554
DB	181	ACATGAACCACTGCTACTCCCGGCTGGCGGGAAGTGTACCCGGAGTCCCGAGAGGCACTC	240
QY	555	AGCTTAGCCAGGTGGAATCTTACAGCGGTCATGCACTACATCTCGACTGCAAGTAG	614
DB	241	AGCTTAGCCAGGTGGAATCTTACAGCGGTCATGCACTACATCTCGACTGCAAGTAG	300
QY	615	TCTGGGCGAGCCAGCCCTCTGAGACCCCTGATGGCCCCCACCCTTCCATCCAGACGCCG	674
DB	301	TCTGGGCGAGCCAGCCCTCTGAGACCCCTGATGGCCCCCACCCTTCCATCCAGACGCCG	360
QY	675	AGCTGCTCCCGGAATCTTGCATCTCCAGCAAAAGAGCTTTGGCACTGACCTCGGCC	734
DB	361	AGCTGCTCCCGGAATCTTGCATCTCCAGCAAAAGAGCTTTGGCACTGACCTCGGCC	420
QY	735	GTGTCTTGA	743
DB	421	GTGTCTTGA	429

Search completed: December 18, 2004, 20:42:47
Job time : 710.883 secs

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OM nucleic - nucleic search, using sw model

Run on: December 18, 2004, 15:00:58 ; Search time 4379.17 Seconds
(without alignments) 10010.347 Million cell updates/sec

Title: US-09-996-529A-5

Perfect score: 1203
Sequence: 1 gatctggggtctgcgcagga.....ttaactttcataaagct 1203

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 1821985908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: gb_ests1:*
2: gb_ests2:*
3: gb_hnc:*
4: gb_ests3:*
5: gb_ests4:*
6: gb_ests5:*
7: gb_ests6:*
8: gb_gsa1:*
9: gb_gsa2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	865.4	71.9	924	1	AL558926
2	865.4	71.9	933	1	AL541035
3	862.2	71.7	924	3	CR597388
4	862.2	71.7	933	3	CR611504
5	862.2	71.7	944	3	CR615457
6	861.6	71.6	944	5	BX458306
7	860.6	71.5	1162	7	CF455737
8	849.2	70.6	943	4	BM916329
9	840.2	69.8	897	3	CR612668
10	837.6	69.6	901	6	CD105185
11	836.4	69.5	912	5	BQ228009
12	834.4	69.4	962	5	BU146429
13	833.6	69.3	1000	4	BM915798
14	831.2	69.1	943	5	BQ278726
15	830	69.0	898	1	AL551330
16	829.4	68.9	984	4	BM474363
17	824.4	68.5	1031	4	BM811433
18	820.4	68.2	1045	4	BM471485
19	818.8	68.1	1020	4	BM541973
20	818.8	68.1	1023	4	BM912688
21	812.8	67.6	910	4	BM801595
22	812.8	67.6	937	5	BQ942011
23	811	67.4	986	4	BM477713
24	808.2	67.2	898	5	BU161821

25	806.8	67.1	954	4	BM553062
26	802.8	66.7	1044	4	BM915317
27	802	66.7	1066	1	AL551484
28	802	66.7	1037	4	BM809010
29	801	66.6	1044	4	BM558277
30	799.8	66.5	1065	4	BM423840
31	798.4	66.4	937	5	BQ432408
32	797.6	66.3	1000	4	BM559173
33	796.8	66.2	1003	4	BM541804
34	794.6	66.1	854	5	BU179445
35	787.8	65.5	836	5	BQ673836
36	782	65.0	894	5	BU508601
37	781.6	65.0	819	4	BG761440
38	780.8	64.9	1053	4	BM477872
39	780.6	64.9	875	6	CD390092
40	779.2	64.8	916	5	BQ681632
41	779.2	64.8	1053	4	BM803498
42	777.4	64.6	1107	4	BM803610
43	776.2	64.5	1090	4	BM541892
44	776	64.5	861	1	AL558925
45	775.6	64.5	985	4	BM557861

ALIGNMENTS

RESULT 1
LOCUS AL558926 924 bp mRNA linear EST 02-APR-2004
DEFINITION Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED
Homo sapiens cDNA clone CS0DJ007YA07 5-PRIME, mRNA sequence.

ACCESSION AL558926
VERSION AL558926.3 GI:46184313
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE

AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 15, 2001 this sequence version replaced gi:31283059.

Contact: Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo (dt) primer. Five cloned end enriched, double-strand cDNA was digested with NotI and cloned into the NotI and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library this sequence belongs to sequence cluster 951.r

For more information about this cluster, see
http://www.genoscope.cns.fr/cdna78=CS0DJ007YA04Qp1&c=951.r.

FEATURES

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/notes="1st strand cDNA was primed with a NotI-oligo (dt) primer. Five prime end enriched, double-strand cDNA was digested with NotI and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 71.9% ; Score 865.4 ; DB 1 ; Length 924 ;
Best Local Similarity 99.7% ; Pred. No. 8.4e-225 ;

[illegible]

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.	1 (bases 1 to 933)	Lj.W.B., Gruber,C., Jessse,J. and Polayes,D.	Full-length cDNA libraries and normalization	Unpublished (2001)
	On Feb 15, 2001 this sequence version replaced gi:30544817.			
	Contact: Genoscope			
	Genoscope Centre National de Sequencage			
	Bp 191 91006 EVRY cedex - France			
	Email: sequef@genoscope.cns.fr, Web : www.genoscope.cns.fr			
	1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prim			
	into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library			
	was not normalized. Library was constructed by Life Technologies,			
	division of Invitrogen.			
	This sequence belongs to sequence cluster 951.r			
	For more information about this cluster, see			
	http://www.genoscope.cns.fr/cdna?e=CS0DE05A11QPlac=951.r.			
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	with a NotI-oligo(dT) primer. Five prime end enriched,			
	double-strand cDNA was digested with Not I and cloned into			
	the Not I and EcoRV sites of the pCMVSPORT 6 vector.			
	Library was not normalized."			
ORIGIN				
Query Match	71.9%	Score 865.4;	DB 1;	Length 933;
Best Local Similarity	99.7%;	Pred. No. 8.4e-225;		
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QY	374	GCGCTGAGCCCGGCTGCGGCTGCTACGAGCGGTGTCTCCCTGTGGAGACGAGCTCG	433	
DB	73	GCGCTGAGCCCGGCTGCGGCTGCTACGAGCGGTGTCTCCCTGTGGAGACGAGCTCG	122	
QY	434	GCCATCGCCCGGCGCCGAGGAGAGCGCCGCGAGCTGAGAGCCGCTGAGCTTCTTGAC	493	
DB	133	GCCATCGCCCGGCGCCGAGGAGAGCGCCGCGAGCTGAGAGCCGCTGAGCTTCTTGAC	192	
QY	494	GACATGAACCACTGTACTCTCCGCTTGGGGAACTGTATCCCGAGATCCCGAGAGCACT	553	
DB	193	GACATGAACCACTGTACTCTCCGCTTGGGGAACTGTATCCCGAGATCCCGAGAGCACT	252	
QY	554	CAGCTTGACGAGGAGGAAATCTCAACGCGGTATAGATCACTATCTTCCGACTGACGTA	613	
DB	253	CAGCTTGACGAGGAGGAAATCTCAACGCGGTATAGATCACTATCTTCCGACTGACGTA	312	
QY	614	GTCTTGCGCAGGCGAGCCCTGTGAGCCCTGATGAGGCCCACTTCCCATCCGAGAGGCC	673	
DB	313	GTCTTGCGCAGGCGAGCCCTGTGAGCCCTGATGAGGCCCACTTCCCATCCGAGAGGCC	372	
QY	674	GAGCTGCTCCCGGAACCTTGTCACTTCCAAACGACAAAAGAGCTTTTGGCACTGACTCGCG	733	
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QY	794	CTTCTCTGCGGAGCGGAGCGGAGGATGGGCCCACTTTCGCTGCGCCACTTGAC	853	
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 RESULT 3
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 LOCUS full-length cDNA clone CS0D007YA07 of T cells (Jurkat cell line)
 DEFINITION CR597388
 ACCESSION CR597388
 VERSION CR597388.1 GI:50478195
 KEYWORDS HTC; cDNA.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE
 AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished
 REMARK Contact: Feng Liang Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Parada Avenue 2 (bases 1 to 924)
 REFERENCE
 AUTHORS Genoscope.
 TITLE Direct Submission
 JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
 COMMENT
 - Web : www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen.
 FEATURES
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0D007YA07"
 /release_type="T cells (Jurkat cell line) Cot
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 Query Match 71.7%; Score 862.2; DB 3; Length 924;
 Best Local Similarity 99.4%; Pred. No. 6.3e-224;
 Matches 886; Conservative 0; Mismatches 3; Indels 2; Gaps 2;
 314 GGACTTCTTTGGTTTCTTTCTTTGGGGGACCTGGACTCACTCCCGCATGAG 373
 |||||||

Db 4 GGACTTCTTTGTTTCTTTCTTTTGGGGGACCTGTGACTCACTCCCGCATGAG 63
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 Db 304 GTTCTGGCGGAGCGAGCCCTGTGAGCCCTGTGAGCCCTGTGAGCCCTGTGAGCC 363
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 Db 843 AAGGTACTTCTGTACATGCGATGTATATTAACCTTTTATAAAGTT 893
 RESULT 4
 CR611504 933 bp mRNA linear HTC 21-JUL-2004
 LOCUS full-length cDNA clone CS0D005YA21 of Placenta of Homo sapiens
 DEFINITION CR611504
 ACCESSION CR611504
 VERSION CR611504.1 GI:50492311
 KEYWORDS HTC; cDNA.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE
 AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/Invitroden Corporation 1600
Faraday Avenue
2 (bases 1 to 933)
REFERENCE Genoscope.
AUTHORS Direct Submission
JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 Evry cedex - FRANCE (E-mail : sequef@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
source location/Qualifiers
1..933
/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="CS0DE005YA21"
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ORIGIN
Query Match 71.7%; Score 862.2; DB 3; Length 933;
Best Local Similarity 99.4%; Pred. No. 6.3e-224;
Matches 886; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

314 GGACTCTTTTGGTTTCTTCTTTGGGCACTTGAAGTCTCCCGAGATGAG 373
13 GAACTCTTTTGGTTTCTTCTTTGGGCACTTGAAGTCTCCCGAGATGAG 72
374 GCGCTGAGCCCGGTGCGGCTGCTACAGAGCGGTGCTGCTGCGAAGAGAGCTG 433
73 GCGCTGAGCCCGGTGCGGCTGCTACAGAGCGGTGCTGCTGCGAAGAGAGCTG 132
434 GCGATGCGCCCGGGGCGAGGAAAGGCGCGGAGCTGAGAGAGCTGAGTGTGAGC 493
133 GCGATGCGCCCGGGGCGAGGAAAGGCGCGGAGCTGAGAGAGCTGAGTGTGAGC 192
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193 GACATGAACCACTGCTACTCCCGCGGAGAACTGTACCCGAGTCCCGAGAGGACT 252
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313 GTCTGCGCGAGAGCGAGCCCTTGAAGCCCTTGAAGCCCTTGAAGCCCTTGAAGCC 372
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1094 GTTGCCCTGATTTTGAAGAGCTATATATAG-GTATATAGTTTGTACTTTTATACAGG 1152
793 GTTGCCCTGATTTTGAAGAGCTATATATAGAGATATATAGTTTGTACTTTTATACAG 851
1153 AAGGTACTTTTCTGTAACTGCAATGCAATGATATATATTAAGTTTATTAAGTT 1203
852 AAGGTACTTTTCTGTAACTGCAATGCAATGATATATTAAGTTTATTAAGTT 902

RESULT 5
LOCUS CR615457 944 bp mRNA linear HTC 21-JUL-2004
DEFINITION Full-length cDNA clone CS0DE001YJ19 of Placenta of Homo sapiens
(human).
ACCESSION CR615457
VERSION CR615457.1 GI:50496264
KEYWORDS HTC; CNSIT_CDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS L4.W.B., Gruber,C., Jesse,J. and Polyes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/Invitroden Corporation 1600
Faraday Avenue
2 (bases 1 to 944)
REFERENCE Genoscope.
AUTHORS Direct Submission
JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 Evry cedex - FRANCE (E-mail : sequef@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
source location/Qualifiers
1..944
/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="CS0DE001YJ19"
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/plasmid="pCMVSPORT_6"

ORIGIN
Query Match 71.7%; Score 862.2; DB 3; Length 944;
Best Local Similarity 99.4%; Pred. No. 6.3e-224;
Matches 886; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

314 GGACTCTTTTGGTTTCTTCTTTGGGCACTTGAAGTCTCCCGAGATGAG 373
8 GGACTCTTTTGGTTTCTTCTTTGGGCACTTGAAGTCTCCCGAGATGAG 67
374 GCGCTGAGCCCGGTGCGGCTGCTACAGAGCGGTGCTGCTGCGAAGAGAGCTG 433
68 GCGCTGAGCCCGGTGCGGCTGCTACAGAGCGGTGCTGCTGCGAAGAGAGCTG 127
434 GCGATGCGCCCGGGGCGAGGAAAGGCGCGGAGCTGAGAGAGCGCTGAGCTTGTGAGC 493
128 GCGATGCGCCCGGGGCGAGGAAAGGCGCGGAGCTGAGAGAGCGCTGAGCTTGTGAGC 187

494 GACATGAACACGACTGCTACTCCGCGCTGGGGAACTGTACCCGGAGTCCCGAGAGGCACT 553
 188 GACATGAACACGACTGCTACTCCGCGCTGGGGAACTGTACCCGGAGTCCCGAGAGGCACT 247
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 248 CAGCTTGGCAGAGTGAATACTCTACACGCGCTGATCGACTAGATTCTCGACCTGCAGGTA 307
 614 GTCTGTGGCGAGGCGAGCCCTTGAACCCCTGATGGCCCCACCTTCCATCCAGACAGCC 673
 308 GTCTGTGGCGAGGCGAGCCCTTGAACCCCTGATGGCCCCACCTTCCATCCAGACAGCC 367
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 Db 847 AAGGTACTTTCTGTAAACATGCGATGTATTTAACTTTTATTAAGTT 897

RESULT 6
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 VERSION BX458306.2 GI:47051752
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 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 1 (bases 1 to 944)
 Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 On May 22, 2003 this sequence version replaced gi:31021015.
 Contact: Genoscope
 Centre National de Sequencage
 BP 191 91006 Evry cedex - France
 Email: seque@genoscope.cns.fr, Web : www.genoscope.cns.fr
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 For more information about this cluster, see
 http://www.genoscope.cns.fr/cdna?b=CSDBE001CE10QP1&c=951.r.

FEATURES

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 with a NotI-oligo(dT) primer. Five prime end enriched,
 double-strand cDNA was digested with Not I and EcoRV sites of the pCMVSPORT 6 vector.
 Library was not normalized."

ORIGIN

Query Match 71.6%; Score 861.6; DB 5; Length 944;
 Best Local Similarity 99.1%; Pred. No. 9.2e-224;
 Matches 883; Conservative 3; Mismatches 3; Indels 2; Gaps 2;

QY 314 GACTCTTTTGTGTTTCTTTCTTTGGGGCACTCTGAGCTCACTCCAGACGTAAAG 373
 Db 8 GACTCTTTTGTGTTTCTTTCTTTGGGGCACTCTGAGCTCACTCCAGACGTAAAG 67
 QY 374 GCGCTGAACCCCGGTCGCGGCTGCTACAGAGCGGTGTCTGCTGCGGAAAGCAGTGTG 433
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 QY 434 GCCATGCCCCGGGCGGAGGAAAGGCCCGGACGTGAGAGCCGCTGAGCTTGTGAC 493
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 QY 614 GTCTGTGGCGAGGCGAGCCCTTGAACCCCTGATGGGCCCACTTCCATCCAGACAGCC 673
 Db 308 GTCTGTGGCGAGGCGAGCCCTTGAACCCCTGATGGGCCCACTTCCATCCAGACAGCC 367
 QY 674 GAGCTCGCTCCGGAACTGTGATCTTCCACAGCAAAAGAGCTTTGGCACTGACTGGC 733
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 Db 428 CGTGTCTGACACCTTCAGACGACAGTGTGGCGCCGCTTGTGCTGGGAGCCCGGAGA 487
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 Db 488 CCTTCTCTGCGGAAAGCCGAGCGGAGTGGGCCCACTTGCCTTGCCTGCGCACTTGAC 547
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 QY 914 GTAGCTGAAGAGCCAGAGCTAGCTGTGGCCACAGCTGGGAGAGTCACTGCTGCCA 973
 Db 608 GTAGCTGAAGAGCCAGAGCTAGCTGTGGCCACAGCTGGGAGAGTCACTGCTGCCA 667
 QY 974 CCCACCCCCCAAGTTCTAAGTCTTTTCAAGGCTGAGAGTGTGAAGAGTGGCTGCTC 1033
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QY 1034 TCCAACTATGCGCAGGCGGCGAGAGCTGTCTTCTGTCTCTTGAAGAAAGTTCT 1093
DB 728 TCCAACTATGCGCAGGCGGCGAGAGCTGTCTTCTGTCTCTTGAAGAAAGTTCT 787
QY 1094 GTTGCCTGATTTTGAAGCTATTAATAG-GTATATAGGTTTTGTACCTTTTAAAGG 1152
DB 788 GTTGCCTGATTTTGAAGCTATTAATAGGTTTTGTACCTTTTAAAGG 846
QY 1153 AAGGTGACTTCTGTACAAATGCGATGTATTAATCTTTTAAAGTT 1203
DB 847 AAGGTGACTTCTGTACAAATGCGATGTATTAATCTTTTAAAGTT 897

RESULT 7
CF455737 1162 bp mRNA linear EST 04-SEP-2003
LOCUS AGENCOURT 15364529 lupski_anterior_horn Homo sapiens cDNA clone
DEFINITION IMAGE:30515866 5', mRNA sequence.
ACCESSION CF455737
VERSION CF455737.1 GI:34455393
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1162)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLES National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgabs-remail.nih.gov
Tissue Procurement: Dr. James R. Lupski
CDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ULNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ULNL at:
http://image.llnl.gov
Plate: NDAM581 row: k column: 11
High quality sequence start: 9
High quality sequence stop: 873.

FEATURES
source Location/Qualifiers

1..1162
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30515866"
/issue_type="Peripheral Nervous system"
/lab_host="DH10B (TI phage-resistant)"
/clone_1ib="lupski anterior horn"
/note="Vector: pCMV-SPORT6.1; Site 1: EcoRV (destroyed);
Site 2: NotI; Library is oligo-dT primed and directionally
cloned (EcoRV site is destroyed upon cloning). Average
insert size 2.1 kb. Library was constructed by Invitrogen
and donated by J. Lupski, M.D./Ph.D. (Baylor College of
Medicine)."

ORIGIN

Query Match 71.5%; Score 860.6; DB 7; Length 1162;
Best Local Similarity 99.3%; Pred. No. 1.8e-223;
Matches 885; Conservative 0; Mismatches 4; Indels 2; Gaps 2;
QY 314 GGAATCTTTTGGTTTCTTCTCTTTGGGACCTGTGACTCACTCCGAGATGAG 373
DB 37 GGAATCTTTTGGTTTCTTCTCTTTGGGACCTGTGACTCACTCCGAGATGAG 96
QY 374 GCGCGAAGCCCGGCGGCGGCGCTGCTAGAGCGGCTGCTGCTGCGAAGCGAGCTG 433
DB 97 GCGCGAAGCCCGGCGGCGGCGCTGCTAGAGCGGCTGCTGCTGCGAAGCGAGCTG 156

QY 424 GCATCGCCCGGAGCGGAGGAGGAGCCGAGCTGAGAGAGCCGCTGAGCTTGAGAC 493
DB 157 GCATCGCCCGGAGCGGAGGAGGAGGAGCCGAGCTGAGAGAGCCGCTGAGCTTGAGAC 216
QY 494 GACATGAACCACTGCTACTCCCGGCTGCGGGAATCTGTTACCCGAGTCCGAGGCACT 553
DB 217 GACATGAACCACTGCTACTCCCGGCTGCGGGAATCTGTTACCCGAGTCCGAGGCACT 276
QY 554 CAGCTTACCGAGTGAATCTCTACAGCGGCTCATCTGACTACATCTTCGAGCTGCAAGTA 613
DB 277 CAGCTTACCGAGTGAATCTCTACAGCGGCTCATCTGACTACATCTTCGAGCTGCAAGTA 336
QY 614 GTCTTGGCGGAGCCAGGCGCCCTGAGACCCCTGATGAGCCCACTTCCATCCAGAGACC 673
DB 337 GTCTTGGCGGAGCCAGGCGCCCTGAGACCCCTGATGAGCCCACTTCCATCCAGAGACC 396
QY 674 GAGCTCGCTCCGGAACCTGTCTATCTCCAGAGCAAAAGAGCTTTGGCCATGACTCGGC 723
DB 397 GAGCTCGCTCCGGAACCTGTCTATCTCCAGAGCAAAAGAGCTTTGGCCATGACTCGGC 456
QY 734 CTGTCTGACACCTCCAGAACGAGGCTGAGCGCCGTTCTGCTGAGGACCCGAGAA 793
DB 457 CTGTCTGACACCTCCAGAACGAGGCTGAGCGCCGTTCTGCTGAGGACCCGAGAA 516
QY 794 CCTCTCGGCGGAGAGCCGAGAGGATGAGGCCCCCACTTGCCCTGCGCACTTGAC 853
DB 517 CCTCTCGGCGGAGAGCCGAGAGGATGAGGCCCCCACTTGCCCTGCGCACTTGAC 576
QY 854 TTCACCAATCCCTTCTGAGACTAAACCTGTGCTCAGAGCGAAGAGCTGTGAACCTT 913
DB 577 TTCACCAATCCCTTCTGAGACTAAACCTGTGCTCAGAGCGAAGAGCTGTGAACCTT 636
QY 914 GTAGCTGAAGAGCCAGAGCTGCTGTGCGCACAGCTGAGCGACCTGCTGCCA 973
DB 637 GTAGCTGAAGAGCCAGAGCTGCTGTGCGCACAGCTGAGCGACCTGCTGCCA 696
QY 974 CCCACCCCAAGTTCTAAGGTTCTTCAAGGCTGAGAGTGTGAGAGAGTGTGCTGCTC 1033
DB 697 CCCACCCCAAGTTCTAAGGTTCTTCAAGGCTGAGAGTGTGAGAGAGTGTGCTGCTC 756
QY 1034 TCCAACTATGCGCAGGCGGCGAGAGCTGTCTTGTGCTCTCTTGGAGAAAGTTCT 1093
DB 757 TCCAACTATGCGCAGGCGGCGAGAGCTGTCTTGTGCTCTCTTGGAGAAAGTTCT 816
QY 1094 GTTGCCTGATTTTGAAGCTATTAATAG-GTATATAGGTTTTGTACCTTTTAAAGG 1152
DB 817 GTTGCCTGATTTTGAAGCTATTAATAGGTTTTGTACCTTTTAAAGG 875
QY 1153 AAGGTGACTTCTGTACAAATGCGATGTATTAATCTTTTAAAGTT 1203
DB 876 AAGGTGACTTCTGTACAAATGCGATGTATTAATCTTTTAAAGTT 926

RESULT 8
BM916329 943 bp mRNA linear EST 12-MAR-2002
LOCUS AGENCOURT 6641978 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5482718
DEFINITION 5', mRNA sequence.
ACCESSION BM916329
VERSION BM916329.1 GI:19366708
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 943)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLES National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: DCTD/DP
CDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: LNCM2009 row: d column: 15
High quality sequence stop: 692.

FEATURES

source

1..943

Location/Qualifiers

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5482718"
/tissue_type="amelanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_41"
/note="Organ: skin; Vector: pOTB7; Site: 1: XhoI; Site: 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

ORIGIN

Query Match 70.6%; Score 849.2; DB 4; Length 943;
Beet Local Similarity 99.2%; Pred. No. 2.2e-220;
Matches 884; Conservative 0; Mismatches 4; Indels 3; Gaps 3;

QY 314 GGAATCTTTTGGTTTCTTCTTTGGGACCTTGATCACTCCCGAGATGAAG 373
DB 1 GGAATCTTTTGGTTTCTTCTTTGGGAG-ACCTTGATCACTCCCGAGATGAAG 59
QY 374 GCGTGAAGCCGCGTGCCTGCTCAAGAGCGGTGTCTGCTGTGCGAAGCATGTG 433
DB 60 GCGTGAAGCCGCGTGCCTGCTCAAGAGCGGTGTCTGCTGTGCGAAGCATGTG 119
QY 434 GCGATCGCCCGGCGGAGGAGGCGCGGACGCTGAGAGCGCTGAGCTTGTGAGC 493
DB 120 GCGATCGCCCGGCGGAGGAGGCGCGGACGCTGAGAGCGCTGAGCTTGTGAGC 179
QY 494 GACATGAACCACTGTGCTACTCCGCGCTGCGGAACTGTACCCGAGATCCCGAGAGCACT 553
DB 180 GACATGAACCACTGTGCTACTCCGCGCTGCGGAACTGTACCCGAGATCCCGAGAGCACT 239
QY 554 CAGCTTAGCAGATGGAATCTTACAGCGCGTCACTGACATCACTTCTGAGCTGAGGTA 613
DB 240 CAGCTTAGCAGATGGAATCTTACAGCGCGTCACTGACATCACTTCTGAGCTGAGGTA 299
QY 614 GTCTGCGGAGCCGAGCCCTTGATGAGCCCTGATGAGCCCTGATCCAGACAGCC 673
DB 300 GTCTGCGGAGCCGAGCCCTTGATGAGCCCTGATGAGCCCTGATCCAGACAGCC 359
QY 674 GAGCTCGCTCGGAACTTGTCACTTCAACGACAAAGAGGTTTGGACATGACTCGGCG 733
DB 360 GAGCTCGCTCGGAACTTGTCACTTCAACGACAAAGAGGTTTGGACATGACTCGGCG 419
QY 734 CGTGTCTGACACCTTCAAGACGAGGTCTGCGCGCCGTTTGTGCTGAGACCCCGGAG 793
DB 420 CGTGTCTGACACCTTCAAGACGAGGTCTGCGCGCCGTTTGTGCTGAGACCCCGGAG 479
QY 794 CTTTCTGCGGAGCCGAGCGGAGGAGTGGGCCCCCACTTGGCCCTGAGCACTTGAAC 853
DB 480 CTTTCTGCGGAGCCGAGCGGAGGAGTGGGCCCCCACTTGGCCCTGAGCACTTGAAC 539
QY 854 TTACACAAATCCCTTCTGAGAGACTAACTGTGTCTGAGAGCGAAGGACTGTGAATCT 913
DB 540 TTACACAAATCCCTTCTGAGAGACTAACTGTGTCTGAGAGCGAAGGACTGTGAATCT 599
QY 914 GTAGCTGAAGACGAGAGCTGTGAGCAACAGCTGGGCGAGTCACTCTGTCTCCA 973
DB 600 GTAGCTGAAGACGAGAGCTGTGAGCAACAGCTGGGCGAGTCACTCTGTCTCCA 659

QY 974 CCCACCCCCCAAGTTCTAAGGTCCTTTTCAGAGCGGTGAGAGGAGGAGGCTGCTC 1033
DB 660 CCCACCCCCCAAGTTCTAAGGTCCTTTTCAGAGCGGTGAGAGGAGGAGGCTGCTC 719
QY 1034 TCACAACTATGCAAGGCGGCGGAGAGAGCTGCTTCTGCTCTCTTGGAGAAAGTTCT 1093
DB 720 TCACAACTATGCAAGGCGGCGGAGAGAGCTGCTTCTGCTCTCTTGGAGAAAGTTCT 779
QY 1094 GTTGCCCTGATTTATGAATCTATATATG-GTATATAGTTTGTGACCTTTTTCACGG 1152
DB 780 GTTGCCCTGATTTATGAATCTATATATAGATATATAGTTTGTGACCTTTTTCACA-CG 838
QY 1153 AAGGACCTTCTGTAACATGCGATGTATTAACCTTTTATTAAGTT 1203
DB 839 AAGGACCTTCTGTAACATGCGATGTATTAACCTTTTATTAAGTT 889

RESULT 9
LOCUS CR612668
DEFINITION Full-length cDNA clone CS0D1064Y612 of Placenta Cot 25-normalized
of Homo sapiens (human).
ACCESSION CR612668
VERSION CR612668.1 GI:50493475
KEYWORDS HTC; CNSLT_cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Li W.B., Gruber C., Jesssee, J. and Polayes D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/Invitrogen Corporation 1600
Faraday Avenue

REFERENCE
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 Evry cedex - FRANCE (E-mail : sequef@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

COMMENT
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.

FEATURES

source

1..897

Location/Qualifiers

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1064Y612"
/tissue_type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"

ORIGIN

Query Match 69.8%; Score 840.2; DB 3; Length 897;
Beet Local Similarity 99.4%; Pred. No. 6.3e-218;
Matches 864; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

QY 336 TCTTTGGGCACTCTGAGCTCACTCCGAGCATGAAGGCGCTGAGCCCGGTGCGCGCT 395
DB 1 TCTTTGGGCACTCTGAGCTCACTCCGAGCATGAAGGCGCTGAGCCCGGTGCGCGCT 60
QY 396 GCTACGAGCGGTGCTGCTGTGAGAGCAGTCTGCGCATCGCCCGGCGGAGGAG 455
DB 61 GCTACGAGCGGTGCTGCTGTGAGAGCAGTCTGCGCATCGCCCGGCGGAGGAG 120
QY 456 AGGGCCCGGAGCTGAGAGCGCGCTGAGCTTGTGAGAGCATGAAACCACTGCTATCC 515
DB 121 AGGGCCCGGAGCTGAGAGCGCGCTGAGCTTGTGAGAGCATGAAACCACTGCTATCC 180

QY 516 GCGTGGGGAACCTGGTACCCGAGTCCCGAGGCACTGACCTTAGCCAGTGGAAATCC 575
Db 181 GCGTGGGGAACCTGGTACCCGAGTCCCGAGGCACTGACCTTAGCCAGTGGAAATCC 240
QY 576 TACAGCCGCTCATGACCTAATCTTCTGACCTTGGAGGTAGCTCTGAGCCAGCCAGCCCTG 635
Db 241 TACAGCCGCTCATGACCTAATCTTCTGACCTTGGAGGTAGCTCTGAGCCAGCCAGCCCTG 300
QY 636 GACCCCTGATGGCCCCCACTTCCCATCCAGACAGCCGAGCTCGCTCCGAACTTGTCA 695
Db 301 GACCCCTGATGGCCCCCACTTCCCATCCAGACAGCCGAGCTCGCTCCGAACTTGTCA 360
QY 696 TCTCCAAACGACAAAGAGCTTTTGGCACTGACCTGCGCGGTGCTGACGACCTCCAGAC 755
Db 361 TCTCCAAACGACAAAGAGCTTTTGGCACTGACCTGCGCGGTGCTGACGACCTCCAGAC 420
QY 756 GCGAGTGTGGCCGCCCTTCTGCTGGAGACCCCGGAGACCTTCTCCGCGAGCCGAGC 815
Db 421 GCGAGTGTGGCCGCCCTTCTGCTGGAGACCCCGGAGACCTTCTCCGCGAGCCGAGC 480
QY 816 GCGAGGATGGGCCCACTTGGCCCTGCGCACTTGAACCTTCAACAAATCCCTTCTGGAG 875
Db 481 GCGAGGATGGGCCCACTTGGCCCTGCGCACTTGAACCTTCAACAAATCCCTTCTGGAG 540
QY 876 ACTAAACCTGTGCTGAGAGCGAGAGCTGTGAACCTTGTAGCTGAGAGCGAGCTA 935
Db 541 ACTAAACCTGTGCTGAGAGCGAGAGCTGTGAACCTTGTAGCTGAGAGCGAGCTA 600
QY 936 GCTCTGGCCACCAAGCTGGGCGACGTCACCTGTCTCCACCCCAACCCCAAGTTCTAAGT 995
Db 601 GCTCTGGCCACCAAGCTGGGCGACGTCACCTGTCTCCACCCCAACCCCAAGTTCTAAGT 660
QY 996 CTCTTTCAGACGCTGAGAGGTGTGAGAGAGTGGCTGTCTCAACATATGCCAAGCGCGC 1055
Db 661 CTCTTTCAGACGCTGAGAGGTGTGAGAGAGTGGCTGTCTCAACATATGCCAAGCGCGC 720
QY 1056 GCGAGCTGTGTCTTCTGCTCTCTTGGAGAAAGTTCTGTGCTCCCTGATTTATGAACCT 1115
Db 721 GCGAGCTGTGTCTTCTGCTCTCTTGGAGAAAGTTCTGTGCTCCCTGATTTATGAACCT 780
QY 1116 ATAAATAG-GTAAATAGT 1174
Db 781 ATAAATAGTAAATAGT 839
QY 1175 CGATGATATTAACCTTTTATTAAGTT 1203
Db 840 CGATGATATTAACCTTTTATTAAGTT 868

RESULT 10
CD105185 901 bp mRNA linear EST 15-MAY-2003
LOCUS CD105185
DEFINITION AGENCOURT 14018727 NIH MGC 179 Homo sapiens cDNA clone
IMAGE:3056955 5', mRNA sequence.
ACCESSION CD105185
VERSION CD105185.1 GI:30758359
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 901)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@db-remail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
cDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNLN at:
http://image.lnl.gov
Plate: NDA4427 row: 6 column: 20
High quality sequence start: 6
High quality sequence stop: 675.
Location/Qualifiers
1. 901
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3036955"
/tissue_type="epituitary"
/lab_host="DH10B-Ton A (T1 and T5 phage resistance)"
/clone_id="NIH-MGC_179"
/note="Organ: brain; Vector: pCMV-sport6.1; Site 1: Scorey (destroyed); Site 2: NotI; Library is oligo-dT primed and directionally cloned (Scorey site is destroyed upon cloning). Average insert size 1.1 kb. Library was constructed by (Invitrogen). Note: this is a NIH-MGC Library."

ORIGIN
Query Match 69.6%; Score 837.6; DB 6; Length 901;
Best Local Similarity 98.3%; Pred. No. 3.3e-217;
Matches 857; Conservative 0; Mismatches 14; Indels 1; Gaps 1;
QY 314 GAACTTTCTTTTGGTTTCTTTCTTTTGGGCACTTGTGACTACTCCAGCATGAAG 373
Db 30 GAACTTTCTTTTGGTTTCTTTCTTTTGGGCACTTGTGACTACTCCAGCATGAAG 89
QY 374 GCGGTGACCCGGGCGCGCTGCTAAGAGCGGTGTGCTGCTGCGAAGCGCACTTG 433
Db 90 GCGGTGACCCGGGCGCGCTGCTAAGAGCGGTGTGCTGCTGCGAAGCGCACTTG 149
QY 434 GCAATGCCCCGGGCGCGAGGAGAGGCGCGCACTGAGAGCGCGTGAAGCTTGAC 493
Db 150 GCAATGCCCCGGGCGCGAGGAGAGGCGCGCACTGAGAGCGCGTGAAGCTTGAC 209
QY 494 GACATGAACACCTGCTACTTCCCGCTGCGGAACTGTATACCCGAGTCCGAGAGCACT 553
Db 210 GACATGAACACCTGCTACTTCCCGCTGCGGAACTGTATACCCGAGTCCGAGAGCACT 269
QY 554 CAGCTTACGAGGTGAAATCTACAGCGCGTATGACATCATCTTGTGACCTGACAGTA 613
Db 270 CAGCTTACGAGGTGAAATCTACAGCGCGTATGACATCATCTTGTGACCTGACAGTA 329
QY 614 GTCTGGCGGAGCGAGCGCCCTGAGATGAGCCCGCACTTCCATTCAGACAGCC 673
Db 330 GTCTGGCGGAGCGAGCGCCCTGAGATGAGCCCGCACTTCCATTCAGACAGCC 389
QY 674 GAGCTGCTCCGGAACCTGTCAATCTCCAAACGACAAAGAGCTTTTGGCACTGACCTGCGC 733
Db 390 GAGCTGCTCCGGAACCTGTCAATCTCCAAACGACAAAGAGCTTTTGGCACTGACCTGCGC 449
QY 734 CGTGTCTGACACCTTCCAGAGCGAGTCTGAGCGCCCTTGTGCTGCGAGACCCCGGAA 793
Db 450 CGTGTCTGACACCTTCCAGAGCGAGTCTGAGCGCCCTTGTGCTGCGAGACCCCGGAA 509
QY 794 CCTCTCTGCGGAGAGCGCGAGCGAGGATGGGCCCAACTTTCGCTGCGCACTTGAC 853
Db 510 CCTCTCTGCGGAGAGCGCGAGCGAGGATGGGCCCAACTTTCGCTGCGCACTTGAC 569
QY 854 TTACCAAAATCCCTTCTTCTGAGACTAACTGTGAGTCTGAGAGCGAGAGCTGTAACTT 913
Db 570 TTACCAAAATCCCTTCTTCTGAGACTAACTGTGAGTCTGAGAGCGAGAGCTGTAACTT 629
QY 914 GTAGCTGAAGAGCGAGACTGCTGTGCGCAACGACTGTGAGCGAGTCACTGTCTCCCA 973
Db 630 GTAGCTGAAGAGCGAGACTGCTGTGCGCAACGACTGTGAGCGAGTCACTGTCTCCCA 689
QY 974 CCCACCCCGCAAGTCTAAAGTCTTTTCAAGCGTGAAGGTGTGAAGAGTGGCTGCTC 1033
Db 690 CCCACCCCGCAAGTCTAAAGTCTTTTCAAGCGTGAAGGTGTGAAGAGTGGCTGCTC 749

QY 1034 TCCAACTATGCGAAGGCGGCGAGAGCTGCTTCTGCTCCCTGGAGAAAGGTTCT 1093
DB 750 TCCAACTATGCGAAGGCGGCGGCGAGAGCTGCTTCTGCTCCCTGGAGAAAGGTTCT 809
QY 1094 GTTGCCCTGATTATGAAGCTATATAG-GTATATAGTTTGTACCTTTTTCACAGG 1152
DB 810 GGTGCCCTGATTATGAAGCTATATAGTATATAGTTTGTACCTTTTTCACAGG 869
QY 1153 AAGGTACTTCTGTATACATGCGATGTATAT 1184
DB 870 AAGGTACTTCTGTATACATGCGATGTATAT 901

RESULT 11
BQ228009 912 bp mRNA linear EST 02-MAY-2002
LOCUS AGENCOURT_7258421 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5786693
DEFINITION 5', mRNA sequence.
ACCESSION BQ228009
VERSION BQ228009.1 GI:20409409
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 912)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bcr-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: LNL12875 row: n column: 06
High quality sequence stop: 607.
Location/Qualifiers
1..912
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5786693"
/tissue_type="leiomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/clone_id="NIH_MGC_71"
/note="Organ: uterus; Vector: pCMV-Sport6; Site: 1: NciI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.1 kb."

ORIGIN
Query Match 69.5%; Score 836.4; DB 5; Length 912;
Best Local Similarity 98.4%; Pred. No. 6.9e-217;
Matches 876; Conservative 0; Mismatches 11; Indels 3; Gaps 3;

QY 314 GAAGCTCTTTGGTTGTTCTCTCTTTGGGCACTGCACTCCCGACGATGAG 373
DB 11 GAAGCTCTTTGGTTGTTCTCTCTTTGGGCACTGCACTCCCGACGATGAG 70
QY 374 GCGCTGAGCCCGGTGCGGCGGTCTACAGAGGCGGTGTCTGCTGCGAAAGCATGCTG 433
DB 71 GCGCTGAGCCCGGTGCGGCGGTCTACAGAGGCGGTGTCTGCTGCGAAAGCATGCTG 130
QY 434 GCCATGCGCCGGGCGGAGGAGGCGCGGAGCTGAGAGAGCCGCTGAGCTTGTGAGC 493
DB 131 GCCATGCGCCGGGCGGAGGAGGCGCGGAGCTGAGAGAGCTTGTGAGCTTGTGAGC 190
QY 494 GACATGAACAAGTACTCCCGCTGCGGGAAGTGTACCCGGAGTCCCGAGAGGCACT 553

DB 191 GACATGAACAAGTACTCCCGCTGCGGGAAGTGTACCCGAGAGTCCCGAGAGCACT 250
QY 554 CAGCTTAGCCAGGTGGAATCTTACAGGCGCTCATCGACTACATTTCTGACTGAGTA 613
DB 251 CAGCTTAGCCAGGTGGAATCTTACAGGCGCTCATCGACTACATTTCTGACTGAGTA 310
QY 614 GTTCCGCGGAGGAGGCGGCGGAGGCGGCGGAGGCGGCGGAGGCGGCGGAGGCGG 673
DB 311 GTTCCGCGGAGGAGGCGGCGGAGGCGGCGGAGGCGGCGGAGGCGGCGGAGGCGG 370
QY 674 GAGCTCGCTCCGGAAGTGTATCTTCAACAGCAAAAGAGCTTTTGCACATGATCGG 733
DB 371 GAGCTCGCTCCGGAAGTGTATCTTCAACAGCAAAAGAGCTTTTGCACATGATCGG 430
QY 734 CGTGCTCTGACACCTCCAGAAAGGAGGCTGCGGCGGCGGCGGCGGCGGCGGAG 793
DB 431 CGTGCTCTGACACCTCCAGAAAGGAGGCTGCGGCGGCGGCGGCGGCGGCGGAG 490
QY 794 CCGTCCGCGGGAAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 853
DB 491 CCGTCCGCGGGAAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 550
QY 854 TTCAACAAATCCCTTCTGAGACTAACTGTGCTCAGAGAGGAGAGGAGTGTGAATT 913
DB 551 TTCAACAAATCCCTTCTGAGACTAACTGTGCTCAGAGAGGAGAGGAGTGTGAATT 610
QY 914 GTAGCTTGAAGAGCCAGAGCTAGCTTGGCCACAGCTGCGGAGCTGACCTGCTCCA 973
DB 611 GTAGCTTGAAGAGCCAGAGCTAGCTTGGCCACAGCTGCGGAGCTGACCTGCTCCA 670
QY 974 CCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAG 1033
DB 671 CCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAG 730
QY 1034 TCCAACTATGCGAAGGCGGCGGAGAGCTGCTTCTGCTCTCTTGGAGAAAGTTCT 1093
DB 731 TCCAACTATGCGAAGGCGGCGGAGAGCTGCTTCTGCTCTCTTGGAGAAAGTTCT 789
QY 1094 GTTGCCCTGATTATGAAGCTATATAGTATATAGTTTGTACCTTTTTCACAGG 1153
DB 790 GTTGCCCTGATTATG-ACCTATATAGATATATAGTTTGTACCTTTTTCACAGG 847
QY 1154 AGGTGACTTCTGTATACATGCGATGTATATATATATATATATATATATAT 1203
DB 848 AGGTGACTTCTGTATACATGCGATGTATATATATATATATATATATATATAT 897

RESULT 12
BUI46429 962 bp mRNA linear EST 03-SEP-2002
LOCUS AGENCOURT_8725408 NIH_MGC_47 Homo sapiens cDNA clone IMAGE:6340250
DEFINITION 5', mRNA sequence.
ACCESSION BUI46429
VERSION BUI46429.1 GI:22659961
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 962)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bcr-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: LNL2536 row: g column: 03

High quality sequence start: 10
High quality sequence stop: 719.
Location/Qualifiers
source

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6340250"
/tissue_type="neuroblastoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_47"
/note="Organ: Brain; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dt priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G) Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 69.4%; Score 834.4; DB 5; Length 962;
Best Local Similarity 96.8%; Pred. No. 2.5e-216;
Matches 872; Conservative 0; Mismatches 27; Indels 2; Gaps 2;

302 GGTCACTGAGC-GGACTCTTTTGGTTTCTTCTTTGGGGAACCTTGGACTCACT 360
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21 GGATCTGAGCGGGCTTTTGGTTTCTTCTTTGGGGAACCTTGGACTCACT 80
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361 CCCGACATGAAGGGCGCTGAGCCCGGTGCGCGCTGCTACGAGCGGTGCTGCTTTC 420
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81 CCCGACATGAAGGGCGCTGAGCCCGGTGCGCGCTGCTACGAGCGGTGCTGCTTTC 140
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421 GGAAGCGACTCTGGCCATGCCCCGGGCGCGAGGAGGGCCCGGCACTGAGAGCCCT 480
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141 GGAAGCGACTCTGGCCATGCCCCGGGCGCGAGGAGGGCCCGGCACTGAGAGCCCT 200
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481 GAGCTTGTGAGCGACATGAACCACTGCTACCTCCGCGTGGGGAACGTGATCCGGAGT 540
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201 GAGCTTGTGAGCGACATGAACCACTGCTACCTCCGCGTGGGGAACGTGATCCGGAGT 260
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541 CCCGAGGCACTGAGCTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 600
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261 CCCGAGGCACTGAGCTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 320
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601 CGAAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 660
|||||
321 CGAAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 380
|||||
661 CATCCAGACGAGCGAGCTGCGTCCGGAACCTTGTCTCTCAACGACAAAGAGCTTTTG 720
|||||
381 CATCCAGACGAGCGAGCTGCGTCCGGAACCTTGTCTCTCAACGACAAAGAGCTTTTG 440
|||||
721 CCAGTACTCGGCGGTGCTCTGACACTTCAGAAAGAGGAGGAGGAGGAGGAGGAGT 780
|||||
441 CCAGTACTCGGCGGTGCTCTGACACTTCAGAAAGAGGAGGAGGAGGAGGAGGAGT 500
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781 GGAAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 840
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501 GGAAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 560
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841 CTGAGCACTGAGCTTCAACCAATCCCTTCTGGAAGCTTAACCTGAGTCTCAAGAGCGAA 900
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561 CTGAGCACTGAGCTTCAACCAATCCCTTCTGGAAGCTTAACCTGAGTCTCAAGAGCGAA 620
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901 GGAAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 960
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621 GGAAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 680
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961 GGAAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 1020
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681 GGAAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 740
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QY 1021 GGAAGCTGAGCTTCAACCAATCCCTTCTGGAAGCTTAACCTGAGTCTCAAGAGCGAA 1080
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DB 741 GGAAGCTGAGCTTCAACCAATCCCTTCTGGAAGCTTAACCTGAGTCTCAAGAGCGAA 800
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QY 1081 GGAAGAGGAGTCTGTTGCGGCTGATTTTGAACCTTATATAGATATA-GGTTTGTAC 1139
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DB 801 GGAAGAGGAGTCTGTTGCGGCTGATTTTGAACCTTATATAGATATAAGGTTTGTAC 860
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QY 1140 CTTTTCACAGGAGGAGTCTTCTGTACATGCAATGCAATGATATATTAACCTTTTATATA 1199
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DB 861 CTTTTCACAGGAGGAGTCTTCTGTACATGCAATGCAATGATATATTAACCTTTTATATA 920
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QY 1200 A 1200
DB 921 A 921

RESULT 13

BM915798 1000 bp mRNA linear EST 12-MAR-2002
LOCUS BM915798
DEFINITION AGENCOURT_6639758 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5482051
ACCESSION AGENCOURT_6639758 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5482051
VERSION BM915798
KEYWORDS BM915798.1 GI:19366177
SOURCE EST.
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 1000)
NIH-MGC <http://mgs.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: gsa@biml.nih.gov
Tissue Procurement: DCTD/DTF

COMMENT

cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
plate: LNCM2007 row: h column: 20
High quality sequence stop: 642.

FEATURES

Location/Qualifiers

1..1000
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5482051"
/tissue_type="amelanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_41"
/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dt priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 69.3%; Score 833.6; DB 4; Length 1000;
Best Local Similarity 97.6%; Pred. No. 4.1e-216;
Matches 867; Conservative 0; Mismatches 19; Indels 2; Gaps 2;

QY 314 GAACTTTTGGTTTCTTCTTTTGGGCACTTGAATCACTCCCAAGATGAAG 373
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DB 12 GAACTTTTGGTTTCTTCTTTTGGGCACTTGAATCACTCCCAAGATGAAG 71
|||||
QY 374 GCAGTACCGCGGTGCGCGCTGCTACGAGCGGTGCTGCTGTGGAACGACATCTG 433
|||||

Db 72 GGGCTGAGGCGCGGTGGCGGCTGCTACGAGCGGTGTGCTGCTGCGAAGCAGACTG 131
Qy 434 GGCATCGCCCGGGGCGGAGGAAAGGCGCGGACGCTGAGAGACCGCTGAGCTTGTGAGC 493
Db 132 GGCATCGCCCGGGGCGGAGGAAAGGCGCGGACGCTGAGAGACCGCTGAGCTTGTGAGC 191
Qy 494 GACATGAACCACTGCTACTCCGCGCTGCGGAACTGTACTCCGAGTCCCGAGAGGCACT 553
Db 192 GACATGAACCACTGCTACTCCGCGCTGCGGAACTGTACTCCGAGTCCCGAGAGGCACT 251
Qy 554 CAGCTTACGCAAGTGAATCTTACAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 613
Db 252 CAGCTTACGCAAGTGAATCTTACAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 311
Qy 614 GTTCCTGCGGAGACCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCG 673
Db 312 GTTCCTGCGGAGACCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCG 371
Qy 674 GAGCTCGCTCGGAGACCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCG 733
Db 372 GAGCTCGCTCGGAGACCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCG 431
Qy 734 CGTGTCTGTGACACTCTGCAAGACGAGGTGCTGCGCGCGCTGCTGCTGCTGCTGCTG 793
Db 432 CGTGTCTGTGACACTCTGCAAGACGAGGTGCTGCGCGCGCTGCTGCTGCTGCTGCTG 491
Qy 794 CTTCTCTGCGCGGAGACCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCG 853
Db 492 CTTCTCTGCGCGGAGACCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCG 551
Qy 854 TTCACCAATCCCTTCTGAGACTTAACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 913
Db 552 TTCACCAATCCCTTCTGAGACTTAACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 611
Qy 914 GTAGCTGAGAGCGCAGAGCTGCTGCGCAACAAGCTGCGGAGCGCTGCTGCTGCTGCTG 973
Db 612 GTAGCTGAGAGCGCAGAGCTGCTGCGCAACAAGCTGCGGAGCGCTGCTGCTGCTGCTG 671
Qy 974 CCCCAACCCCAAGTTCTAAGGTCTTTTCAAGGTGTGAGGTGTGAGGTGTGAGGTGTG 1033
Db 672 CCCCAACCCCAAGTTCTAAGGTCTTTTCAAGGTGTGAGGTGTGAGGTGTGAGGTGTG 731
Qy 1034 TCCAACTATGCGAGCGCGGCGGAGAGCT-GGTCTTGTGCTGCTGCTGCTGCTGCTGCTG 1092
Db 732 TCC-AACTATGCGAGCGCGGCGGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 790
Qy 1093 TGTTCGCCCTGATTTTGAATCTATATATAGTATATAGTATATAGTATATAGTATATAG 1152
Db 791 TGTTCGCCCTGATTTTGAATCTATATATAGTATATAGTATATAGTATATAGTATATAG 850
Qy 1153 AAGGTGACTTTCTGTAACAATGCGATGATATATTAACCTTTTATATAA 1200
Db 851 AAGGTGACTTTCTGTAACAATGCGATGATATATTAACCTTTTATATAA 898

RESULT 14
BQ278726 1043 bp mRNA linear EST 07-MAY-2002
LOCUS AGENCOURT 7049519 NIH_MGC_107 Homo sapiens cDNA clone IMAGE:5805370
DEFINITION 5', mRNA sequence.
ACCESSION BQ278726
VERSION BQ278726.1 GI:20488934
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 1043)
AUTHORS NIH-MGC <http://mgi.mc.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgabbs@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LCM2044 row: h column: 11
High quality sequence stop: 686.
Location/Qualifiers
1..1043
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5805370"
/tissue_type="adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 107"
/note="Organ: breast; Vector: pOT7; Site 1: EcoRI;
Site 2: XhoI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC library."

ORIGIN
Query Match 69.1%; Score 831.2; DB 5; Length 1043;
Best Local Similarity 99.2%; Pred. No. 1.9e-215;
Matches 877; Conservative 0; Mismatches 3; Indels 4; Gaps 4;
Qy 322 TTTGATTTCTTTCTTTGAGGACCTCTGAGCTCACTCCGACAGTAAAGCGCTGAG 381
Db 1 TTTGATTTCTTTCTTTGAGGAG-ACCTGAGCTCACTCCGACAGTAAAGCGCTGAG 59
Qy 382 CCCGCTGCGCGCTCTGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 441
Db 60 CCCGCTGCGCGCTCTGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 119
Qy 442 CCGGCGCGAGGAGGCGCGCGAGCTGAGAGCGCGCTGAGCTTGTGAGAGATGAA 501
Db 120 CCGGCGCGAGGAGGCGCGCGAGCTGAGAGCGCGCTGAGCTTGTGAGAGATGAA 179
Qy 502 CCAGTCTACTCCGCTGCGGAACTGATACCGGAGTCCGAGAGGCACTTCACTTAA 561
Db 180 CCAGTCTACTCCGCTGCGGAACTGATACCGGAGTCCGAGAGGCACTTCACTTAA 239
Qy 562 CCAGTGAATCTTACAGCGGCTGATGATCACTTCTGACCTGCAAGTATGCTTGGC 621
Db 240 CCAGTGAATCTTACAGCGGCTGATGATCACTTCTGACCTGCAAGTATGCTTGGC 299
Qy 622 CGAGCAGCGCGCTGAGCGCGGATGAGCGCGGACCTTCCATCGAGACGCGAGCTGCG 681
Db 300 CGAGCAGCGCGCTGAGCGCGGATGAGCGCGGACCTTCCATCGAGACGCGAGCTGCG 359
Qy 682 TCCGGAATCTTGCATCTCCAGACGACAAAGAGCTTTTGCATGATCTGAGCGCTGCT 741
Db 360 TCCGGAATCTTGCATCTCCAGACGACAAAGAGCTTTTGCATGATCTGAGCGCTGCT 419
Qy 742 GACACTCTCAAGACGAGTGTGCGCGCGCTTCTGCTGCTGAGACCGCGGAACTCTCT 801
Db 420 GACACTCTCAAGACGAGTGTGCGCGCGCTTCTGCTGCTGAGACCGCGGAACTCTCT 479
Qy 802 GCGGAGCGCGAGCGGAGTGGGCGCGCACTTGCCTGCGCCACTTGAATTACCA 861
Db 480 GCGGAGCGCGAGCGGAGTGGGCGCGCACTTGCCTGCGCCACTTGAATTACCA 539
Qy 862 ATCCCTTCTGAGACTTAACTGTGCTCAAGACGAGAGCTGTGAACCTTGAAGCTTG 921
Db 540 ATCCCTTCTGAGACTTAACTGTGCTCAAGACGAGAGCTGTGAACCTTGAAGCTTG 599

QY 922 AAGAGCAGAGCTAGCTGCGCACCAGCTGGGCGACGTCACTGCT-CCGACCCACC 980
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Db 600 AAGAGCAGAGCTAGCTGCGCACCAGCTGGGCGACGTCACTGCT-CCGACCCACC 659
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QY 981 CCCAAGTTTAAAGTCTTTTCAAGCGGTGGAAGAGAGAGTGTCTTCCAAAC 1040
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QY 1041 TATGCAAGCGGCGGAGAGCTGCTCTGCTCCCTTGGAGAAAGTTTCTGTC 1100
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Db 720 TATGCAAGCGGCGGAGAGCTGCTCTGCTCCCTTGGAGAAAGTTTCTGTC 779
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QY 1101 TGAATTATGACTATATATAG-GTATATAGTTTGTACTTTTTCAGGAAAGTGA 1159
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Db 780 TGAATTATGACTATATATAGAGTATAGGTTTGTACTTTTTCAG-GGAAGTGA 838
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QY 1160 CTTTCTGTACAAATGCGATGATATTAACCTTTTATTAAGTT 1203
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Db 839 CTTTCTGTACAAATGCGATGATATTAACCTTTTATTAAGTT 882
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|
|

RESULT 15
AL551330
LOCUS AL551330 898 bp mRNA linear EST 30-MAR-2004
DEFINITION AL551330 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0D1064YG12 5-PRIME, mRNA sequence.
ACCESSION AL551330
VERSION AL551330.3 GI:45856137
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE Li W.B., Gruber C., Jessee J. and Polayes D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 15, 2001 this sequence version replaced gi:31273146.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo (dt) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
951.r

For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?S=CS0D1064BD06QPK=951.r.
FEATURES
source
location/Qualifiers
1..898
/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="CS0D1064YG12"
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/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dt)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 69.0%; Score 830; DB 1; Length 898;
Best Local Similarity 99.2%; Pred. No. 3.9e-215; Indels 3; Gaps 3;
Matches 863; Conservative 2; Mismatches 2; Indels 3; Gaps 3;

QY 336 TCTTTGGGCACTCTGACTCACTCCAGCATGAAGCGCTGAGCCCGGTGCGGCT 395
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Db 1 TCTTTGGGCACTCTGACTCACTCCAGCATGAAGCGCTGAGCCCGGTGCGGCT 60
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|
|
QY 396 GCTACGAGCGGTGTGCTGCTGCGAAGCAGTCTGGCCATGCGCGGGCGAGGGA 455
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|

Db 61 GCTACGAGCGGTGTGCTGCTGCGAAGCAGTCTGGCCATGCGCGGGCGAGGGA 120
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QY 456 AGGCGCCGAGCTGAGAGCGCGTGAAGTCTGGAAGCATGAACCATCTACTCC 515
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Db 121 AGGCGCCGAGCTGAGAGCGCGTGAAGTCTGGAAGCATGAACCATCTACTCC 180
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QY 516 GCTGCGGGAATGAGTACCCGGAATCCCGAAGGCACTCAGCTTACCGAGTGAATCC 575
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Db 181 GCTGCGGGAATGAGTACCCGGAATCCCGAAGGCACTCAGCTTACCGAGTGAATCC 240
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QY 576 TACAGCGGTGATGACTACTCTGACCTGACCTGAGTATGTCCTGAGCAGCCCTG 635
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Db 241 TACAGCGGTGATGACTACTCTGACCTGACCTGAGTATGTCCTGAGCAGCCCTG 300
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|
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QY 636 GACCCCTGATGAGCCCACTTCCATCCAGACAGCCGAGCTGCTCCGGAATTGCA 695
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Db 301 GACCCCTGATGAGCCCACTTCCATCCAGACAGCCGAGCTGCTCCGGAATTGCA 360
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QY 696 TCTCCAGCAAAAGAGAGCTTTGCACTGACCTGCGCGGTGCTGACACCTCCAGAAC 755
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Db 361 TCTCCAGCAAAAGAGAGCTTTGCACTGACCTGCGCGGTGCTGACACCTCCAGAAC 420
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QY 756 GCAAGTGTGCGCGCGCTTCTGCTGCGGAGACCCGGAACCTGCTCCGGAAGCCGAGAC 815
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Db 421 GCAAGTGTGCGCGCGCTTCTGCTGCGGAGACCCGGAACCTGCTCCGGAAGCCGAGAC 480
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QY 876 ACTAAGCTGTGCTGAGAGCGAAGAGCTGGAAGCTTGAAGCTGGAAGCGAGACTA 935
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QY 936 GCTGTGCAACCAAGCTGAGGAGCTCACTGCTCCCAACCCCAAGTTCTAAGT 995
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QY 996 CTTTTCAGAGCGTGAAGTGTGGAAGAGTGTCTCTCCAACTATGCGAAGCGGCG 1055
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QY 1056 GCAGAGCT-GTCTTCTGCTCTCTTGGAGAAAGTTCTGTGCCGATTTAAGATC 1114
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